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(71) Applicant: **KABUSHIKI KAISHA HAYASHIBARA
SEIBUTSU KAGAKU KENKYUJO
Okayama-shi Okayama (JP)**

(72) Inventors:
• **Ario, Takeshi
Okayama-shi, Okayama (JP)**

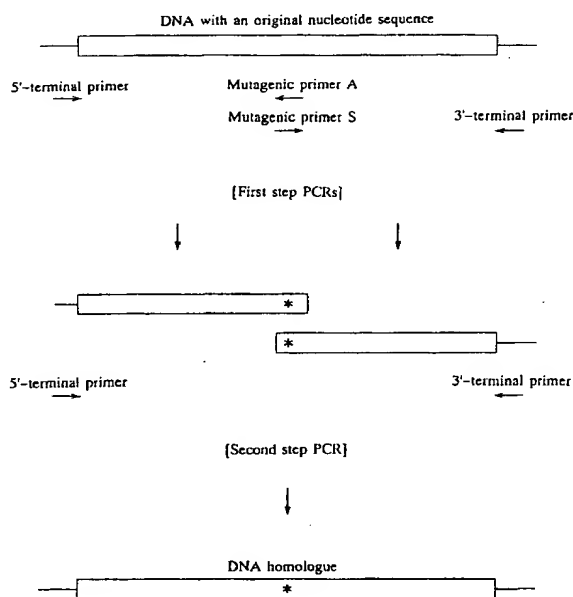
- **Taniai, Madoka
Okayama-shi, Okayama (JP)**
- **Yamamoto, Kozo
Okayama-shi, Okayama (JP)**
- **Kurimoto, Masashi
Okayama-shi, Okayama (JP)**

(74) Representative: **Daniels, Jeffrey Nicholas et al
Page White & Farrer
54 Doughty Street
London WC1N 2LS (GB)**

(54) Polypeptides having L-asparaginase activity

(57) Disclosed are polypeptides which originate from mammal, having L-asparaginase activity. The polypeptides are easily prepared by applying recombinant DNA techniques to DNAs encoding the polypep-

tides and they exert satisfactory effects in the treatment and/or the prevention for diseases caused by tumor cells dependent on L-asparagine, and cause no substantial serious side effects even when administered to humans in relatively-high dose.



Note: An asterisk indicates a site where a nucleotide is substituted, and a box indicates a polypeptide-encoding sequence.

FIG.1

Description

The present invention relates to L-asparagine amidohydrolytic enzymes, more particularly, to polypeptides which originate from mammal, having L-asparaginase activity.

L-Asparaginase (EC 3.5.1.1) is an enzyme which catalyzes the hydrolytic reaction of L-asparagine into L-aspartic acid and ammonia. The studies on the antitumor activity of L-asparaginase started from the following reports: J. G. Kidd et al. described the inhibitory action of guinea pig sera on cells of lymphomas in *"The Journal of Experimental Medicine"*, Vol.98, pp.565-582 (1953), and J. D. Broome et al. evidenced in *"Nature"*, Vol.191, pp.1,114-1,115 (1961), that the L-asparaginase activity of the guinea pig sera was responsible for the inhibitory action. It is now understood that the inhibitory action is caused by the lack of L-asparagine, an essential nutrient to proliferate and survive for some tumor cells which defect L-asparagine synthetase activity, such as acute lymphocytic leukemia, but not for normal cells. The hydrolysis of L-asparagine by L-asparaginase in patients with such tumor cells induces selective death of the tumor cells, resulting in the treatment of malignant tumors.

L-Asparaginase has been studied energetically for its actual use as an antitumor agent, and one derived from *Escherichia coli* is now in use as a therapeutic agent for leukemia and lymphoma. However, L-asparaginase from *Escherichia coli* is merely an external protein for human, and repetitive administration of conventional compositions with such L-asparaginase may cause serious side effects such as anaphylaxis shock, urticaria, edema, wheeze and dyspnea. These compositions are inevitably restricted with respect to administration dose and frequency. Therefore, some proposals to reduce or even diminish such side effects have been given.

As a first proposal, Japanese Patent Kokai No.119,082/79 discloses a chemically modified L-asparaginase from *Escherichia coli*, in which at least 65 % amino acids are blocked with 2-O- substituted polyethylene glycol-4,6-dichloro-S-triazine. As a second proposal, human L-asparaginases are disclosed in Japanese Patent Kokai Nos.320,684/92 and 19,018/80, where the L-asparaginases are respectively obtained from cultures of human cell lines and human urine. While the first proposal has an advantage of that the L-asparaginase from *Escherichia coli* is easily obtainable on an industrial scale, it has a disadvantage of that the modifying reaction is difficult to control and the side effects couldn't be eliminated completely. While the second proposal has an advantage of that unlike L-asparaginase from *Escherichia coli*, the L-asparaginases from human may not substantially induce antibodies even when administered to patients, it has a disadvantage of that it is not easy to obtain the L-asparaginases in a desired amount by the processes disclosed in Japanese Patent Kokai Nos.320,684/92 and 19,018/80.

Recently, recombinant DNA technology has advanced remarkably. If a DNA which encodes a desired polypeptide is once isolated, it is relatively easy to obtain a transformant which produces the polypeptide by constructing a recombinant DNA, comprising the DNA and a self-replicable vector, followed by introducing the recombinant DNA into a host, such as a microorganism, animal- or plant-cell. The polypeptide is obtainable in a desired amount from the culture of the transformant. However, no DNA which encodes mammalian L-asparaginase was isolated, and no mammalian L-asparaginase was produced by recombinant DNA techniques.

Therefore, it has been in great demand to isolate DNAs which encode active L-asparaginases originating from mammal and establish processes to prepare the L-asparaginases on a large-scale by applying the recombinant DNA techniques to the isolated DNAs.

In view of foregoing, the first object of the present invention is to provide a polypeptide which originates from mammal, having L-asparaginase activity.

The second object of the present invention is to provide a DNA which encodes the polypeptide.

The third object of the present invention is to provide a recombinant DNA which containing a DNA which encodes the polypeptide and a self-replicable vector.

The fourth object of the present invention is to provide a transformant obtainable by introducing a DNA which encodes the polypeptide into a host.

The fifth object of the present invention is to provide a process to prepare the polypeptide by using the transformant.

The sixth object of the present invention is to provide an agent for susceptible diseases, containing the polypeptide as an effective ingredient.

The first object of the present invention is attained by polypeptides which originate from mammal, having L-asparaginase activity.

The second object of the present invention is attained by DNAs which encode the polypeptides.

The third object of the present invention is attained by recombinant DNAs containing DNA which encode the polypeptides and a self-replicable vector.

The fourth object of the present invention is attained by transformants obtainable by introducing the DNAs into appropriate hosts.

The fifth object of the present invention is attained by a process to prepare the polypeptides which comprises culturing the transformants and collecting the produced polypeptides from the resultant cultures.

The sixth object of the present invention is attained by agents for susceptible diseases, containing the polypeptides

as effective ingredients.

FIG. 1 is a scheme of the over lap extension method.

FIG. 2 is a restriction map of the present recombinant DNA pKGPA/WT.

FIG. 3 is a scheme of the preparation of the present recombinant DNA pBIgGPA/WT.

FIG. 4 is a restriction map of the present recombinant DNA pBIgGPA/WT.

FIG. 5 is a restriction map of the present recombinant DNA pKGPA/D364stp.

FIG. 6 is a restriction map of the present recombinant DNA pKHA/MUT1.

FIG. 7 is a restriction map of the present recombinant DNA pKHA/MUT2.

FIG. 8 is a restriction map of the present recombinant DNA pKHA/MUT3.

FIG. 9 is a restriction map of the present recombinant DNA pKHA/MUT3.

FIG. 9 is a restriction map of the present recombinant DNA pKHA/MUT5.

FIG. 10 is a restriction map of the present recombinant DNA pBIgGPA/D364stp.

FIG. 11 is a restriction map of the present recombinant DNA pBIgHA/MUT1.

FIG. 12 is a restriction map of the present recombinant DNA pBIgHA/MUT2.

FIG. 13 is a restriction map of the present recombinant DNA pBIgHA/MUT3.

FIG. 14 is a restriction map of the present recombinant DNA pBIgHA/MUT4.

Explanation of the symbols are as follows:

The symbols, "Eco RI", "Hind III", "Not I" and "Xho I", indicate cleavage sites by restriction enzymes, *Eco RI*, *Hind III*, *Not I* and *Xho I*, respectively.

The symbols, "D364stp", "HA/MUT1", "HA/MUT2", "HA/MUT3" and "HA/MUT5", indicate DNAs encoding the present polypeptides.

The symbol "Ptac" indicates a Tac promotor.

The symbol "rrnBT12" indicates a region for transcriptional termination, derived from a ribosomal RNA operon.

The symbol "AmpR" indicates an ampicillin resistant gene.

The symbol "pBR322ori" indicates a replication origin in *Escherichia coli*.

The symbol "Ig sec" indicates a DNA encoding a polypeptide with a signal sequence for secretion of immunoglobulin.

The symbol "Emsv" indicates an enhancer from long terminal repeats of Moloney Mouse Sarcoma Virus.

The symbol "Pmti" indicates a promotor for Mouse metallothionein I gene.

The symbol "Poly (A)" indicates a polyadenylation signal derived from SV40 virus.

The symbol "BPV1" indicates a genome of a bovine *papillomavirus*.

The present inventors isolated mammalian DNAs encoding L-asparaginases firstly in the world, from guinea pig and human, and succeeded in elucidating their nucleotide sequences. The nucleotide sequences of the DNAs from a guinea pig and human are in SEQ ID NOs:15 and 16, respectively. This information is disclosed in Japanese Patent Application No.42,564/95 (Japanese Patent Kokai No.214,885/96) by the same applicant of this application. The present invention has been made based on the above information, and provides the polypeptides which originate from mammal, having L-asparaginase activity.

The polypeptides of the present invention are not restricted to their sources or origins so far as they originate from mammal and have an L-asparaginase activity. The polypeptides are usually obtainable by the expression of genes originating from mammal, and usually contain amino acid sequences of SEQ ID NOs:1 to 3, wherein the symbol "Xaa" in SEQ ID NO:3 means "glutamine" or "arginine". For example, the polypeptides have any one of amino acid sequences of SEQ ID NOs:4 to 9. In view of the technical level in this field, one or more amino acid residues in SEQ ID NOs:4 to 9 can be substituted relatively easily by different ones without substantial defects of the activity. Despite derived from the same DNA, a variety of polypeptides with an L-asparaginase activity may be obtained as a result of modifications by endogenous enzymes of the hosts after the DNA expression or modifications during purification of the polypeptides, depending on the types of vectors and hosts used to obtain transformants or culturing conditions of the transformants, such as ingredients, compositions, temperatures or pHs. The wording "a variety of polypeptides" includes the polypeptides with deletions and/or additions of one or more amino acids at the N- and/or C-termini thereof, or with glycosylations. In view of these, the present polypeptides include not only the polypeptide with any amino acid sequence of SEQ ID NOs:4 to 9 but also their homologues so long as they have an L-asparaginase activity. The present polypeptides express the activity when exist in multiple forms, preferably, tetramers.

The polypeptides of the present invention can be usually prepared by the recombinant DNA techniques. In general, the polypeptides are obtainable by culturing transformants containing DNAs encoding the polypeptides and collecting the produced polypeptides from the resultant cultures. The transformants are obtainable by introducing such recombinant DNAs as contain any one of the nucleotide sequences of SEQ ID Nos:10 to 15 and a self-replicable vector into appropriate hosts. One or more nucleotides in SEQ ID NOs:10 to 15 can be substituted by different nucleotides without substantial changes of the encoding amino acid sequences with respect to degeneracy of genetic code. To facilitate the expression of the DNA in the hosts, one or more nucleotides in nucleotide sequences which encode the polypeptides

or their homologues can be appropriately substituted by different ones. Furthermore, nucleotide sequences which encode and/or don't encode one or more amino acids can be added to the 5'- and/or 3'-termini of the nucleotide sequences.

The DNAs encoding the polypeptides of this invention include those from natural sources and those synthesized artificially so far as the polypeptides expressed by them have an L-asparaginase activity. The DNAs can be wild-type ones, containing the same nucleotide sequences as those from natural sources, and can be their homologues.

Examples of the wild-type DNAs include DNAs containing the nucleotide sequences of SEQ ID NOs:15. The wild-type DNA is obtainable from natural sources such as guinea pig livers, as disclosed in Japanese Patent Application No.42,564/95 (Japanese Patent Kokai No.214,885/96) by the same applicant of this invention: (a) constructing a cDNA library by applying usual methods to purified poly (A)⁺ RNAs from a guinea pig or human liver as materials, (b) applying the plaque hybridization method to the cDNA library using oligonucleotides as probes synthesized chemically based on partial amino acid sequences of L-asparaginase purified from a guinea pig serum, (c) collecting phage clones containing the DNAs encoding the polypeptides of this invention, and (d) manipulating the collected phage clones in a conventional manner. The wild-type DNA can be synthesized chemically based on SEQ ID NO:15.

Examples of DNA homologues to the wild-type ones include DNAs containing any nucleotide sequence of SEQ ID NOs:10 to 14. DNA homologues containing the nucleotide sequence of SEQ ID NO:10 are obtainable by applying conventional methods in this field, such as PCR method and methods for site-directed mutagenesis, to the wild-type DNA of SEQ ID NO:15 concerning the desired sequence. DNA homologues containing any nucleotide sequence of SEQ ID NOs:11 to 14 are obtainable by the methods such as follows: Firstly, A wild-type DNA with the nucleotide sequence of SEQ ID NO:16 is obtained by the methods as disclosed in Japanese Patent Application No.42,564/95 (Japanese Patent Kokai No.214,885/96) by the same applicant of this invention, i.e., screening a human liver cDNA library. Subsequently, the wild-type DNA is subjected to conventional methods as mentioned above concerning desired sequences to obtain the DNA homologues. The DNA homologues can be synthesized chemically based on the nucleotide sequences of SEQ ID NOs:10 to 14.

The present DNAs can be generally introduced into hosts as in forms of recombinant DNAs. In general, each recombinant DNA comprises one of the present DNAs and a self-replicable vector. The recombinant DNAs can be easily prepared by general recombinant DNA techniques when the DNAs are available. Examples of such self-replicable vectors include pKK223-3, pGEX-2T, pRL- λ , pBTrp2 DNA, pUB110, YEpl3, Ti plasmid, Ri plasmid, pBI121, pCDM8, pBPV and BCMGSneo. Among these vectors, pKK223-3, pGEX-2T, pRL- λ , pBTrp2 DNA pUB110 are suitably used to express the present DNAs in prokaryotic cells such as *Escherichia coli* and *Bacillus* sp., while YEpl3, Ti plasmid, Ri plasmid, pBI121, pCDM8, pBPV and BCMGSneo are suitably used to express the present DNAs in eukaryotic cells such as yeasts and animal- and plant-cells.

To insert the present DNAs into the vectors, conventional methods in this field can be arbitrarily used. Examples of such methods contain the steps of (a) cleaving self-replicable vectors with restriction enzymes, (b) introducing the same cleavage sites, by the same restriction enzymes as used to cleave the vectors, to the 5'- and 3'- termini of the present DNAs by applying polymerase chain reaction to form double-stranded DNAs, (c) cleaving the double-stranded DNAs by the restriction enzymes, and (d) ligating the cleaved vectors with cleaved DNAs by the action of DNA ligases. The recombinant DNAs thus obtained can be easily introduced into appropriate hosts, resulting in limitless replication of the DNAs by culturing the transformants.

The recombinant DNAs according to the present invention can be introduced into appropriate hosts such as *Escherichia coli*, *Bacillus* sp., actinomycetes, yeasts and plant- and animal-cells. To introduce the DNAs into *Escherichia coli*, it can be cultured in the presence of the recombinant DNAs and calcium ion. To introduce them into *Bacillus* sp., competent cell methods or protoplast methods can be used. To introduce them into animal-cells, DEAE-dextran methods or electroporation methods can be used. Desired transformants can be cloned by applying hybridization methods or by selecting L-asparaginase producing cells from the cultures.

The transformants thus obtained produce the present polypeptides intracellularly or extracellularly when cultured in nutrient culture media. Examples of such media are usually liquid nutrient culture media which generally contain carbon sources, nitrogen sources and minerals, and further contain micronutrients such as amino acids and/or vitamins on demand. The carbon sources usable in the present invention include saccharides such as starch, starch hydrolysates, glucose, fructose and sucrose. The nitrogen sources usable in the present invention include organic and inorganic compounds containing nitrogen, such as ammonia and their salts, urea, nitrates, peptone, yeast extract, defatted soy bean, corn steep liquor and beef extract. Cultures containing the present polypeptides can be obtained by inoculating the transformants into the above media, culturing them at temperatures of 25-65°C at pHs of 5-8 for about 1-10 days under aerobic conditions by aeration-agitation method, etc.

The cultures can be used intact as agents for susceptible diseases. However, the cultures are usually treated with ultrasonication or cell wall lytic enzymes to disrupt cells, and the present polypeptides are separated by using techniques such as filtration and centrifugation from the cell-disruptants and purified. Alternatively, the polypeptides can be purified from the culture supernatants obtained by removing cells from the cultures by filtration or centrifugation,

etc. The present polypeptides can be purified by applying techniques generally used in this field for protein purifications, such as salting out, dialysis, filtration, concentration, gel filtration chromatography, ion-exchange chromatography, affinity chromatography, hydrophobic chromatography, isoelectric focusing and gel electrophoresis, and if necessary, two or more of them can be applied combination to the supernatants which are separated from insoluble substances of cell-disruptants, or to the culture supernatants. The resultant purified solutions polypeptides can be concentrated and/or lyophilized into liquids or solids depending on their final uses.

The following experiments explain the present invention in more detail, and the techniques used therein are conventional ones in this field: For example, the techniques are disclosed by J. Sambrook et al. in "*Molecular Cloning, A Laboratory Manual*", 2nd edition (1989), published by Cold Spring Harbor Laboratory Press, New York, U.S.A., and by Masami MATSUMURA in "*Laboratory Manual for Genetic Engineering*" (1988), published by Maruzen Co., Ltd., Tokyo, Japan.

Experiment 1

Expression of wild-type DNA

Experiment 1-1

Expression of guinea pig wild-type DNA

Experiment 1-1(a)

Preparation of guinea pig wild-type DNA

A guinea pig wild-type DNA encoding L-asparaginase was prepared by the method disclosed in Japanese Patent Kokai No.214,885/96 by the same applicant of this invention. The DNA had the nucleotide sequence of SEQ ID NO: 15. A DNA having a polypeptide-encoding region in SEQ ID NO:15, i.e., a sequence of containing the nucleotides 20-1,714 in SEQ ID NO:15, is called "GPA/WT DNA" hereinafter, and the expression product thereof with the amino acid sequence of SEQ ID NO:15 is called "guinea pig wild-type L-asparaginase". SEQ ID NO:17 shows in parallel the nucleotide sequence of GPA/WT DNA and the amino acid sequence encoded thereby.

Experiment 1-1(b)

Preparation of recombinant DNA

Ten μ l of 10 x PCR buffer, one μ l of 25 mM dNTP mix, one ng of the human wild-type DNA, obtained in Experiment 1-1(a), as a template were placed in 0.5 ml reaction tube. The mixture was mixed with, as a sense- and anti-sense-primers, an adequate amount of an oligonucleotide chemically synthesized based on the amino acid sequences near the N- and C- termini of SEQ ID NO:15, volumed up with sterilized distilled water to give a total volume of 99.5 μ l, and mixed with 0.5 μ l of 2.5 units/ μ l of AmpliTaq DNA polymerase. The nucleotide sequence of the sense primer was 5'-AATCTCGAGCCACCATGGCGCGCATCA-3', a nucleotide sequence obtained by adding a common nucleotide sequence in animal cells, as shown by M. Kozak in "*Nucleic Acid Research*", Vol.15, pp.8,125-8,148 (1987), to the upstream of a region which encodes the N-terminal amino acid sequence of SEQ ID NO:15 and then adding to the further upstream a cleavage site by a restriction enzyme, *Xho* I. The nucleotide sequence of the anti-sense primer was 5'-CTGCGGCCGCTTATCAGATGGCAGCGGCAC-3' as a complement to a nucleotide sequence obtained by adding two termination codons to the downstream of a region which encodes the C-terminus of the amino acid sequence of SEQ ID NO:15 and adding a cleavage site by a restriction enzyme, *Not* I, to the further downstream. The resulting mixture was successively incubated at 94°C for one min, at 55°C for one min, and at 72°C for 3 min, and the series of incubation was repeated 40-times for PCR to amplify DNA. Thus, a DNA containing GPA/WT DNA was obtained and then cleaved by restriction enzymes of *Xho* I and *Not* I to obtain an about 1.7 kbp DNA fragment. Twenty-five ng of the DNA fragment was weighed and mixed with 10 ng of a plasmid vector, "pCDM8", commercialized by Invitrogen Corporation, San Diego, U.S.A., which had been cleaved by restriction enzymes of *Xho* I and *Not* I. To the DNA mixture thus obtained was added an equal volume of the solution I in "LIGATION KIT VERSION 2" commercialized by Takara Shuzo, Tokyo, Japan, and incubated at 160C for 2 hours to obtain a replicable recombinant DNA, "pCGPA/WT".

The recombinant DNA pCGPA/WT was introduced into an *Escherichia coli* MC1061/P3 strain, commercialized by Invitrogen Corporation, San Diego, U.S.A., by competent cell method. The transformant thus obtained was inoculated into L broth medium (pH 7.2) containing 20 μ g/ml ampicillin and 10 μ g/ml tetracycline followed by cultivation at 37°C for 18 hours under shaking conditions. The transformants were collected from the culture by centrifugation and sub-

jected to conventional alkali-SDS method to extract the recombinant DNA pCGPA/WT. The analysis of the pCGPA/WT by an automatic sequencer equipped with a fluorophotometer confirmed that it contained GPA/WT DNA, which termination codons were ligated to the 3'-terminus and was ligated to the downstream of a CMV promotor from the 5'- to 3'-termini.

The system using COS-1 (ATCC CRL-1650) as a host, which is a cell line derived from a monkey kidney, was used to express the DNA in the following Experiments 1 and 2. Since the system is for a transient expression, it has a disadvantage that DNAs introduced into transformants could not be stable over several days, and the transformants do not produce the desired polypeptides repeatedly. However, it is known that the number of copies of the desired DNA per cell temporally increases to 10^5 when plasmid vectors having a replication origin derived from SV40 virus, such as the above mentioned pCDM8, are introduced into the COS-1 cells. With this point of view, the system has a merit that it quite easily analyzes the desired DNA-expression product.

Experiment 1-1(c)

Recombinant DNA expression in COS-1 cell

In accordance with the DEAE-dextran method reported by Frederick M. Ausubel et al. in "*Current Protocols in Molecular Biology*" (1987), chapters 9.2.1-9.2.3 and 9.2.5-9.2.6, published by John Wiley and Sons Inc., New York, U. S.A., the recombinant DNA pCGPA/WT in Experiment 1-1(b) was introduced into COS-1 cells for its expression. To each well of "3046", a plastic multiwell plate, with 6 wells of 3.5 cm diameter, commercialized by Becton Dickinson Labware, New Jersey, U.S.A., was added 2.5 ml of DME medium, containing 10 v/v % bovine fetal serum and 1.8×10^5 COS-1 cells. The cells were cultured at 37°C in a 5 v/v % CO₂ incubator overnight. After removing the culture supernatant by an aspirator and washing the remaining cells with DME medium containing 50 mM Tris-HCl buffer (pH 7.4), each well was charged with 2.5 ml of DME medium containing 2.8 µg/ml PCGPA/WT, 50 mM Tris-HCl (pH 7.4), 0.4 mg/ml DEAE-dextran and 0.1 mM chloroquine, and incubated at 37°C for 4 hours in a 5 v/v % CO₂ incubator. Thereafter, the culture supernatant was removed, and the remaining cells in each well were received with 2.5 ml of 10 mM phosphate buffered saline (hereinafter abbreviated as "PBS") containing 10 v/v % DMSO before incubating at ambient temperature for 2 minutes. After removing the supernatant and washing the remaining cells with DME medium containing 50 mM Tris-HCl (pH 7.4), each well was charged with 2.5 ml of "COS MEDIUM", commercialized by COSMO BIO CO. LTD., Tokyo, Japan, followed by cultivation at 37°C for 3 days in a 5 v/v % CO₂ incubator to express the desired DNA. As a control, the same experiment was carried out using a plasmid vector, pCDM8.

After 3 days' cultivation, the multiwell plates with the cultures were subjected thrice to a treatment of freezing at -80°C and thawing at ambient temperature to disrupt the cells. The whole cultures were transferred to centrifugal tubes and centrifuged to remove insoluble components after precipitated, followed by obtaining total soluble fractions, concentrating the fractions using membranes, and adjusting the volume of the total soluble fraction per well to give 0.5 ml for the following analyses.

Experiment 1-1(d)

Assay for L-asparaginase activity

L-Asparaginase activity was expressed by the unit assayed as follows: Samples were placed in 1.5 ml-reaction tubes in 50 µl each and admixed with 200 µl of 50 mM phosphate buffer (pH 7.0) containing 1.4 mg/ml L-asparagine. After standing at 37°C for 0, 1, 2, 4, 6 and 16 hours, L-aspartic acid in the reaction mixtures was quantified by an amino acid analyzer. In parallel, 1.0, 0.5 and 0.25 unit/ml dilutions of an L-asparaginase from *Escherichia coli* were provided and quantified for L-aspartic acid after incubating at 37°C for 0 and one hour, and based on the increased amount of L-aspartic acid, a calibration curve was drawn. By plotting on the calibration curve the increased amounts of L-aspartic acid of the samples, the samples' L-asparaginase activities were estimated. The activity of samples with a lower activity was estimated based on that assayed after 2 hours or more incubation. One unit activity of L-asparaginase was defined as the amount that releases one µmol of ammonia from L-asparagine per minute under the above conditions.

The total soluble fractions obtained in Experiment 1-1(c) were treated similarly as above, and expressed their activities as total L-asparaginase activities that were detected in the soluble fractions from 1.8×10^5 COS-1 cells. As a result, the activity of the total soluble fraction in Experiment 1-1(c) was 0.083 unit, and the control gave no activity.

Experiment 1-1(e)Western blotting

5 An anti-L-asparaginase antibody was prepared as follows: An oligopeptide of a sequence Gly-Ser-Gly-Asn-Gly-Pro-Thr-Lys-Pro-Asp-Leu-Leu-Gln-Glu-Leu-Arg-Cys was synthesized chemically in a usual manner. Keyhole Limped Hemocyanin was linked to the C-terminus of the oligopeptide. The resultant was purified and used to immunize rabbits in a usual manner. The rabbits were immunized 6 times 2 weeks about, then the whole blood was collected and subjected to salting out with 50 w/v % ammonium sulfate to obtain an anti-L-asparaginase anti-serum.

10 In accordance with the method reported by U. K. Laemli et al. in *"Nature"*, Vol.227, pp.680-685 (1970), 0.2 ml of the total soluble fraction in Experiment 1-1(c) was subjected to 12.5 w/v % SDS-polyacrylamide gel electrophoresis (hereinafter abbreviated as "SDS-PAGE"). The polypeptides migrated were transferred to a nitrocellulose membrane and subjected to Western blotting using the above anti-L-asparaginase anti-serum, in accordance with the method reported by H. Towbin in *"Proceedings of the National Academy of Sciences of the U.S.A."*, Vol.76, pp.4,350-4,354
15 (1979). For color development, alkaline phosphatase system was used. Comparing with the control and molecular weight markers, both the identification of bands specifically stained in the sample and the measurement of the molecular weight of each subunit of the L-asparaginase were carried out. The molecular weight markers used were bovine serum albumin (67 kDa), ovalbumin (45 Kda), soy bean trypsin inhibitor (20.1 kDa) and α -lactalbumin (14.4 kDa), and stained with amide black. The total soluble fraction in Experiment 1-1(c) gave no clear band.

Experiment 1-1(f)Measurement of molecular weight on gel filtration

25 Two ml of the total soluble fraction in Experiment 1-1(c) was subjected to gel filtration column chromatography using "HILOAD SUPERDEX 200 COLUMN", with an inner diameter of 16 mm and a length of 60 cm, commercialized by Pharmacia LKB Biotechnology AB, Uppsala, Sweden, equilibrated with PBS. Based on the L-asparaginase activity of the eluted fractions, the molecular weight of the guinea pig wild-type L-asparaginase in a native form was examined. The molecular weight markers used were thyroglobulin (699 kDa), ferritin (440 kDa), catalase (232 kDa), aldolase (158
30 kDa), bovine serum albumin (67 kDa) and ovalbumin (43 kDa). The peak of L-asparaginase activity in the eluted fractions was observed in a position corresponding to a molecular weight of about 300 kDa.

Since no clear band was detected by Western blotting, the molecular weight of the wild-type L-asparaginase in a dissociated form could not be detected, while the molecular weight in a native form was estimated to be about 300 kDa based on the result of gel filtration. The molecular weights of L-asparaginase in a native and dissociated form, purified from guinea pig L-asparaginase in serum, were respectively estimated to be about 190 kDa on gel filtration
35 and about 43 kDa on DS-PAGE. As disclosed in Japanese Patent Kokai No.214,885/96 by the same applicant of the present invention, 3 partial amino acid sequences of a guinea pig L-asparaginase in serum were observed in a region of amino acids 10-236 in the sequence of guinea pig wild-type L-asparaginase. While, two consensus amino acid sequences essential for the expression of L-asparaginase activity, i.e., SEQ ID NOs:1 and 2, as proposed by E. Harms in *"FEBS letters"*, Vol.285, pp.55-58 (1991) based on the results of experiments on L-asparaginase derived from *Es-*
40 *cherichia coli*, correspond to the sequences of amino acids 16-19 and 114-118 in the amino acid sequence of the guinea pig wild-type L-asparaginase. In view of these and the results in Experiment 1-1, the present inventors estimated that the guinea pig wild-type L-asparaginase may require a region of amino acids about 1-400 in the amino acid sequence to express the activity. In Experiment 2-1, to examine the L-asparaginase activities of C-terminal defective
45 mutants as homologues of the guinea pig wild-type L-asparaginase, the expression products of DNA homologues from a guinea pig were tested for properties and features.

Experiment 1-2Expression of human wild-type DNA

50 A human wild-type DNA encoding L-asparaginase was prepared according to the method in Japanese Patent Kokai No.214,855/96 by the same applicant of the present invention. The DNA had the nucleotide sequence of SEQ ID NO:16. Hereinafter, a DNA having a polypeptide-encoding region in SEQ ID NO:16, i.e., a sequence of nucleotides
55 93-1,811 in SEQ ID NO:16, was named "HAWT DNA", and a polypeptide, as the expression product of HAWT DNA, having the amino acid sequence of SEQ ID NO:16, may be called "human wild-type L-asparaginase". SEQ ID NO:18 shows the nucleotide sequence of GPA/WT DNA and the amino acid sequence encoded thereby.

Except for the template and the sense- and anti-sense-primers, PCR was performed under the same conditions

as used in Experiment 1-1(b). As a template, the human wild-type DNA in Experiment 1-2 was used. As a sense- and anti-sense-primers, oligonucleotides with sequences of 5'-AATCTCGAGCCACCATGGCGCGCGG GTG-3' and 5'-CTGCGGCCGCTTATCAGACACCAGGCAGCAC-3' were respectively used. The DNA thus amplified was continuously treated with the same method as used in Experiment 1-1(b) to prepare a recombinant DNA, "pCHA/WT". After sequencing, the pCHA/WT was introduced into COS-1 cells and expressed followed by analyzing the expression product similarly as in Experiment 1-1.

In contrast to the guinea pig wild-type L-asparaginase, the experiment system could not detect the human wild-type L-asparaginase activity. It was presumably due to that the human wild-type L-asparaginase had a lower specific activity than that of the guinea pig wild-type one, and this forced to examine the properties of expression products by DNA homologues from human in Experiment 2-2.

Experiment 2

Expression of DNA homologue

Experiment 2-1

Expression of DNA homologue originating from guinea pig

A termination codon was replaced for the nucleotide sequence in a specific position of the guinea pig wild-type DNA to obtain a DNA homologue: A DNA was obtained by PCR method by replacing a termination codon for a codon of the nucleotides 1,090-1,092 or 1,012-1,014 in SEQ ID NO:17. Except for the nucleotide sequence of anti-sense primer, PCR was performed under the same conditions as used in Experiment 1-1(b). As an anti-sense primer, an oligonucleotide with a sequence of 5'-CTGCGGCCGCTTATCATGCCGTGGGCAGTGT-3' or 5'-CTGCGGCCGCTTAT-CAGCCCAACACGTAGGA-3' was used to prepare the two-types of DNAs. The amplified DNAs were treated similarly as in Experiment 1-1(b) to obtain recombinant DNAs, "pCGPA/D364stp" and "pCGPA/L338stp". By sequencing similarly, it was confirmed that pCGPA/D364stp and pCGPA/L338stp had DNAs, encoding the sequences of amino acids 1-363 and 1-337 in the guinea pig wild-type L-asparaginase, respectively, and had a termination codon at their 3'-termini free of intervening sequences. Hereinafter, the polypeptide-encoding regions of the DNAs are respectively named "GPA/D364stp DNA" and "GPA/L338stp DNA". GPA/D364stp DNA and GPA/L338stp DNA were ligated in the downstream of a CMV promoter in the direction from the 5'- to 3'-termini. The DNAs expression products may be named "guinea pig L-asparaginase homologues".

The above recombinant DNAs were introduced into COS-1 cells and examined similarly as in Experiment 1-1. As controls, pCGPA/WT and pCDM8 in Experiment 1-1(b) were similarly treated and examined. Table 1 shows the results.

Table 1

Recombinant DNA	L-asparaginase activity (unit)	Molecular weight (kDa) *1	Molecular weight (kDa) *2
pCGPA/WT	0.083	-	about 300
pCGPA/D364stp	0.228	about 40	about 140
pCGPA/L338stp	N.D. *3	about 40	-
pCDM8	N.D. *3	-	-

Note: The symbols "*1", "*2" and "*3" mean that the value was determined by Western blotting, the value was determined by gel filtration, and the activity was not detected, respectively.

As shown in Table 1, the activities of the expression products of GPA/WT DNA and GPA/D364stp DNA were detected, but not for GPA/L338stp DNA. These results suggest that a region of amino acids 1-363 in the guinea pig wild-type L-asparaginase may be enough for sufficiently expressing the L-asparaginase activity. This amino acid sequence, amino acids 1-363 in the guinea pig wild-type, is SEQ ID NO:4, and a nucleotide sequence which encodes the

amino acid sequence is SEQ ID NO:10. The amino acid sequence of the guinea pig wild-type L-asparaginase is SEQ ID NO:5.

Experiment 2-2

Expression of DNA homologue originating from human

DNA homologues were prepared by replacing specific codons in the human wild-type DNA with termination codons or codons for different amino acids. The DNA homologues were prepared by replacing termination codons for the nucleotides 1096-1098 in SEQ ID NO:18 by applying PCR method. Except for the template and the sense- and anti-sense-primers, PCR was performed under the same conditions as used in Experiment 1-1(b). As a template, the human wild-type DNA in Experiment 1-2 was used. As a sense- and anti-sense-primers, the oligonucleotides with sequences of 5'-AATCTCGAGCCACCATGGCGCGCGCGGTG-3' and 5'-CTGCGGCCGCTCATTACACCGAGGGTGGCGT-3' were respectively used. The amplified DNA was treated similarly as in Experiment 1-1 to obtain a recombinant DNA, "pCHA/E366stp", and sequenced. It was confirmed that pCHA/E366stp contained a DNA encoding amino acids 1-365 in SEQ ID NO:16 and a termination codon at the 3'-terminus free of intervening sequences. The polypeptide-encoding region was named "HA/E366stp DNA", hereinafter. HA/E366stp DNA was ligated to the downstream of a CMV promoter in the direction from the 5'- to 3'-termini.

To change specific codons in DNAs into ones for different amino acids, the over lap extension method reported by Robert M. Horton et al. in *"Methods in Enzymology"*, Vol.217, pp.270-279 (1993), published by Academic Press, Inc., San Diego, U.S.A., was used. The method is summarized in FIG.1 and explained as follows: First, mutagenic primers A and B, where the nucleotides to be mutagenized were substituted by desired different ones complementary to one another, were prepared. The mutagenic primer A was a sense strand, and the mutagenic primer B was an anti-sense strand. A set of 5'- and 3'-terminal primers, which amplify the whole region of the desired DNA, were prepared, and they were respectively a sense- and anti-sense-strands. Second, conventional PCR was performed using the 5'-terminal primer, the mutagenic primer A, and as a template, a DNA with the original nucleotide sequence. In parallel, another PCR as was performed using the same DNA as a template, the 3'-terminal primer, and the mutagenic primer B. These two PCRs were named "first step PCRs". Third, two DNAs amplified in the first step PCRs were mixed with the 5'- and 3'-terminal primers as used in the first step PCRs followed by performing PCR as a second step PCR. The two DNA fragments amplified in the first step PCRs were used as primers and templates to generate mutagenized DNAs, while the 5'- and 3'-terminal primers were used as primers to amplify the mutagenized DNAs. By this method, DNAs into which were introduced 7 types nucleotide substituents, i.e., 7 DNA homologues were prepared. The 7 types nucleotide substituents and consequent changes of the encoded amino acid sequences are summarized in Table 2. The template DNA and mutagenic primers A and B used to prepare the 7 DNA homologues were summarized in Table 3. The 5'- and 3'-terminal primers were respectively equal to the sense- and anti-sense-primers as used to prepare pCHA/E366stp in Experiment 2-2.

Table 2

DNA homologue	Recombinant DNA	Nucleotide substitution (upper line) and consequential change of amino acid (lower line) *
HA/MUT1 DNA	pCHA/MUT1	C894G, A902G, G952A, G953A and G1096T H298Q, Q301R, G318N and E366stp
HA/MUT2 DNA	pCHA/MUT2	C894G, A902G and G1096T H298Q, Q301R and E366stp
HA/MUT3 DNA	pCHA/MUT3	C894G, G952A, G953A and G1096T H298Q, G318N and E366stp
HA/MUT4 DNA	pCHA/MUT4	A902G, G952A, G953A and G1096T Q301R, G318N and E366stp
HA/MUT5 DNA	pCHA/MUT5	C894G and G1096T H298Q and E366stp
HA/MUT6 DNA	pCHA/MUT6	A902G and G1096T Q301R and E366stp
HA/MUT7 DNA	pCHA/MUT7	G952A, G953A and G1096T G318N and E366stp

*) Numbers in the upper lines in each column mean a nucleotide number in SEQ ID NO:18. Numbers in the lower lines in each column means an amino acid residue number in SEQ ID NO:18. Alphabets on the left and right of the numbers in the upper lines show nucleotides before and after the nucleotide substitution, respectively. Alphabets on the left and right of the numbers in the lower lines show amino acids before and after the nucleotide substitution, respectively. The symbol "stp" means that a termination codon was substituted for a codon in the wild-type DNA. Names for the 7 DNA homologues and the recombinant DNAs containing the DNA homologues are shown in parallel.

Table 3

DNA homologue	Template DNA	Nucleotide sequences of mutagenic primers A (upper line) and B (lower line) *
HA/MUT1 DNA	pCHA/MUT7	the same as used for HA/MUT2 DNA preparation the same as used for HA/MUT2 DNA preparation
HA/MUT2 DNA	pCHA/E366stp	5'-CCCCCGGAGGCAC TGGGT-3' 5'-ACCCAgTGCCTCCgGGG-3'
HA/MUT3 DNA	pCHA/MUT7	the same as used for HA/MUT5 DNA preparation the same as used for HA/MUT5 DNA preparation
HA/MUT4 DNA	pCHA/MUT7	the same as used for HA/MUT6 DNA preparation the same as used for HA/MUT6 DNA preparation
HA/MUT5 DNA	pCHA/E366stp	5'-CCCC TGGAGGCAC TGGGT-3' 5'-ACCCAgTGCCTCCgGGG-3'
HA/MUT6 DNA	pCHA/E366stp	5'-CCCCCGGAGGCAC TGGGT-3' 5'-ACCCACTGCCTCCgGGG-3'
HA/MUT7 DNA	pCHA/E366stp	5'-GACGttGGCTCCCGCCCAT-3' 5'-ATGCGGGGAGCCaaCGTC-3'

Note: Small letters mean nucleotides which were substituted for those in human wild-type DNA.

The obtained DNA homologues from human were treated similarly as in Experiment 1-1 to obtain recombinant DNAs "pCHA/MUT1", "pCHA/MUT2", "pCHA/MUT3", "pCHA/MUT4", "pCHA/MUT5", "pCHA/MUT6" and "pCHA/MUT7". The expression products of the DNA homologues, obtained in Experiment 2-2, may be named "human L-

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asparaginase homologues", hereinafter. After sequencing, these DNA homologues were introduced into COS-1 cells, followed by expression and assay. As controls, pCHA/WT obtained in Experiment 1-2 and pCDM8 were treated and examined. Signal intensities of bands, detected by Western blotting, were evaluated by densitometry to compare quantitatively the expressed products. The results were in Table 4.

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Table 4

Recombinant DNA	L-asparaginase activity (unit) *1	Molecular weight (kDa) *2	Quantity *3	Molecular weight (kDa) *4
pCHA/WT	N.D.	-	-	-
pCHA/E366stp	N.D.	about 40	2.3	-
pCHA/MUT1	0.021	about 40	0.4	about 140
pCHA/MUT2	0.031	about 40	0.9	about 140
pCHA/MUT3	0.009	about 40	0.1	about 140
pCHA/MUT4	N.D.	about 40	0.2	-
pCHA/MUT5	0.006	about 40	1.2	about 140
pCHA/MUT6	N.D.	about 40	1.9	-
pCHA/MUT7	N.D.	about 40	0.2	-
pCDM8	N.D.	-	-	-

Note: The symbols "*1", "*2", "*3" and "*4" mean the activity was not detected, the value was determined by Western blotting, the value indicates the signal intensity of the band detected on Western blotting and quantified by densitometry, and the value was determined by gel filtration, respectively.

The results in Table 4 indicate that human L-asparaginases both in the wild-type and in the C-terminal defected mutant, i.e., the expression product of HAV366stp DNA, as the one of the homologues, had a lower specific activity than that from guinea pigs. In addition, these results indicate that the specific activity of L-asparaginases among those of point mutants, which some of the amino acids inherent to the human wild-type L-asparaginase were substituted by different ones, increased to a detectable level. The human DNA homologues such as HA/MUT1, HA/MUT2, HA/MUT3 and HA/MUT5, which the expression products gave a detectable level of activity, have SEQ ID NOs:11 to 14, respectively, and encoding SEQ ID NOs:6 to 9, respectively.

Based on the results in the above experiments, the present inventors found that polypeptides from mammal may require the amino acid sequence of SEQ ID NO:3 (where the symbol "Xaa" meant "glutamine" or "arginine") to express a detectable level of L-asparaginase activity in the expression and assay systems in Experiments 1 and 2, in addition to conventionally known as such amino acid sequences of SEQ ID NOs:1 and 2. The amino acid sequence of the guinea pig wild-type L-asparaginase contains the SEQ ID NO:3 in the region the amino acids 298-302. Examples of such polypeptides, having all the amino acid sequences of SEQ ID NOs:1 to 3, include those having SEQ ID NOs:4 and 5 from guinea pigs and those having SEQ ID NOs:6 to 9 from human.

Based on the above findings, the present inventors invented the polypeptides having L-asparaginase activity. The following examples explain the present invention, and the techniques used therein are conventional ones used in the art, and of course, they are not restrictive to the present invention: Example A-1 Polypeptides having L-asparaginase activity Example A-1(a)

Preparation of transformant

Ten μ l of 10 x PCR buffer, one μ l of 25 mM dNTP mix, one ng of the recombinant DNA pCGPA/WT DNA obtained in Experiment 1-1 as a template, and an adequate amount of oligonucleotides as a sense- and anti-sense-primers synthesized chemically based on the 5'- and 3'-terminal sequences of GPA/WT DNA were placed in 0.5 ml reaction tube. The mixture was mixed with sterilized distilled water to give a total volume of 99.5 μ l, and 0.5 μ l of 2.5 units/ μ l AmpliTaq DNA polymerase were further added. The sequence of the sense primer was 5'-GCGAATTCATGGCGCGCG-CATCA-3' which was a nucleotide sequence obtained by adding a cleavage site by a restriction enzyme, *Eco* RI, to the upstream of the 5'-terminus of GPA/WT DNA. The sequence of the anti-sense primer was 5'-GCAAGCTTTCAGATGGCAGGCGGCAC-3', which was complementary to a nucleotide sequence prepared by adding a termination codon to the 3'-terminus of GPA/WT DNA and then adding a cleavage site by a restriction enzyme, *Hin* dIII, to the downstream. The above mixture was subjected to 40 cycles of successive incubations at 94°C for one min, at 55°C for one min, and 72°C for 3 min to perform PCR. By cleaving the amplified DNA by restriction enzymes *Eco* RI and *Hin* dIII, a *Eco* RI-*Hin*-dIII fragment with a length of about 1.7 kbp was obtained. Twenty-five ng of the DNA was mixed with 10 ng of plasmid vector "pKK223-3", commercialized by Pharmacia LKB Biotechnology AB, Uppsala, Sweden, which had been cleaved by restriction enzymes *Eco* RI and *Hin* dIII, and then mixed with the solution I in "LIGATION KIT VERSION 2" commercialized by Takara Shuzo Inc., Tokyo, Japan, in an equal volume of the DNA mixture, followed by incubation at 160°C for 2 hours to obtain a replicable recombinant DNA, "pKGPA/WT".

The recombinant DNA pKGPA/WT was introduced into an *Escherichia coli* strain "JM105" by the competent cell method. The resulting transformant "J-GPA/WT" was inoculated to L broth medium (pH 7.2) containing 50 μ g/ml ampicillin and cultured at 37°C for 18 hours under shaking conditions. The transformants collected by centrifugation from the culture were subjected to a conventional alkali-SDS method to extract the recombinant DNA pKGPA/WT. As shown in FIG.2, analysis using an automatic sequencer equipped with a fluorophotometer revealed that GPA/WT DNA of SEQ ID NO:17 ligated to the downstream of a Tac promotor in the direction from the 5'- to 3'-termini. In addition, it was confirmed that a termination codon was ligated to the downstream of GPA/WT DNA without intervening sequences.

Example A-1(b)

Production of polypeptide

The transformant J-GPA/WT was inoculated into L broth medium (pH 7.2), containing 50 μ g/ml ampicillin, and cultured at 37°C for 18 hours under shaking conditions to obtain a seed culture. Eighteen L of a fresh preparation of the same medium was placed in a 30-L jar fermenter, inoculated with one v/v % of the seed culture, and cultured at 37°C under aeration-agitation conditions. A portion of the culture was placed in a cuvette with 1-cm in thickness, incubated until the absorbance at a wavelength of 650 nm reached to about 1.5, admixed with IPTG to give a final concentration of 0.1 mM, and incubated for 5 hours. The cells centrifugally collected from the culture were suspended in a mixture solution (pH 7.2) containing 139 mM NaCl, 7 mM Na_2HPO_4 and 3 mM NaH_2PO_4 , and supersonicated to disrupt the cells, followed by centrifuging the resultant to obtain a supernatant.

Ammonium sulfate was added to the supernatant under ice-chilling conditions to give a concentration of 50 w/v %

and then dissolved to homogeneity. After standing for several minutes, the precipitates were collected by centrifugation, dissolved in 20 mM Tris-HCl buffer (pH 8.0), and dialyzed against a fresh preparation of the same buffer followed by applying the dialyzed solution to "Q SEPHAROSE FF COLUMN", commercialized by Pharmacia LKB Biotechnology AB, Uppsala, Sweden, equilibrated with the same buffer. After washing sufficiently with the same buffer, the column was fed with a linear gradient buffer of NaCl increasing from 0 M to 0.5 M in 20 mM Tris-HCl buffer (pH 8.0). The fractions eluted at about 0.1-0.3 M NaCl were collected, and the solvent was replaced with 10 mM sodium-phosphate buffer (pH 7.5) while concentrating with membranes. The concentrated solution was then applied to "L-ASPARAGINE AGAROSE", commercialized by Sigma Chemical Co., St. Louis, U.S.A., equilibrated with the same buffer. After washing with the same buffer, 10 mM sodium phosphate buffer (pH 7.5) containing 0.5 M NaCl was fed to the column for elution. The eluted fractions were pooled and concentrated by using a membrane. The concentrate was applied to "HILOAD SUPERDEX 200 COLUMN", commercialized by Pharmacia LKB Biotechnology AB, Uppsala, Sweden, equilibrated with Tris-HCl buffer (pH 8.0) containing 10 v/v % glycerol, and eluted from the column. The eluted fractions, containing substances with a molecular weight of about 300 kDa, were collected to obtain a purified polypeptide with a purity of 90% or more in a yield of about 0.1 mg/ml culture.

Example A-1(c)

Physicochemical property of polypeptide

The purified polypeptide in the above was analyzed to determine the physicochemical properties: The molecular weight of the purified polypeptide in a native form was determined by gel filtration similarly as in Experiment 1-1(e). The peak for L-asparaginase activity of the eluted fractions was found at a position corresponding to a molecular weight of about 300 kDa. The molecular weight of the purified polypeptide in a dissociated form was determined by SDS-PAGE as used in Experiment 1-1(e). The main band was observed at a position corresponding to a molecular weight of about 50±10 kDa. The results indicate that the purified polypeptide exists in a multimer as a native form. Considering errors in measurement by the above methods and the fact that all the known L-asparaginases from *Escherichia coli* etc., other than mammal, exist in a tetrameric form, it can be estimated that the purified polypeptide exists in a tetrameric form. The method as used in Experiment 1-1(d) confirmed that the purified polypeptide has an L-asparaginase activity.

Example A-2(a)

Preparation of transformant

FIG.3 summarizes the procedures to prepare transformants. PCR was performed under the same conditions as used in Example A-1(a) except for the nucleotide sequences of a sense- and anti-sense-primers. As the sense- and anti-sense-primers, oligonucleotides with the nucleotide sequences of 5'-GTGAATTCGGAGGTTTCAGATGGCGCGCGCATCA-3' and 5'-CTGCGGCCGCTCAGATGGCAGGCGGCAC-3' were respectively used. The DNA thus amplified was cleaved by restriction enzymes *Eco* RI and *Not* I to obtain an about 1.7 kbp *Eco* RI-*Not* I fragment. Seventy ng of the DNA fragment was mixed with 50 ng of a plasmid vector, "pBPV", commercialized by Pharmacia LKB Biotechnology AB, Uppsala, Sweden, cleaved in advance by restriction enzymes *Xho* I and *Not* I, and 25 ng of each of 4 oligonucleotides as linkers with nucleotide sequences of 5'-TCGAGCCACCATGAAGTGTTCGTGGGTTATT-3', 5'-TTCTTCCTGATGGCCGTAGTGACAGGAGTG-3', 5'-AATTCACCTCCTGTCACACGGCCATCAGGA-3', and 5'-AGAAAATAACCCACGAACACTTCATGGTGGC-3'. The oligonucleotides for linkers were synthesized in a usual manner and used after reacted with T4 polynucleotide kinase, commercialized by Pharmacia LKB Biotechnology AB, Uppsala, Sweden, and purified by ethanol-precipitation. To the DNA mixture was added the solution I in "LIGATION KIT VERSION 2", commercialized by Takara Shuzo, Tokyo, Japan. The mixture was incubated at 16°C for 2 hours to obtain a replicable recombinant DNA "pBlgGPA/WT".

The recombinant DNA pBlgGPA/WT was introduced into an *Escherichia coli* HB101 strain by the competent cell method. The transformant thus obtained was inoculated into L broth medium (pH 7.2) containing 50 µg/ml ampicillin followed by cultivation at 37°C for 18 hours under shaking conditions. The transformants, collected by centrifuging the resulting culture, were subjected to a conventional alkali-SDS method to extract the recombinant DNA pBlgGPA/WT. The nucleotide sequence analysis using an automatic sequencer confirmed that the recombinant DNA pBlgGPA/WT had the structure in FIG.4: A DNA encoding a polypeptide containing a signal sequence for immunoglobulin secretion, as shown by D. F. Stern et al. in "Science", Vol.235, pp.321-324 (1984), i.e., "Ig sec DNA" was ligated to the downstream of a region for transcriptional regulation, comprising an enhancer derived from long terminal repeats of Moloney Mouse Sarcoma Virus (Emsv), and a promoter derived from Mouse metallothionein I gene (Pmti). Furthermore, GPA/WT DNA was ligated in the same frame to the downstream of the Ig sec DNA in the direction from the 5'- to 3'-termini of GPA/WT DNA. It was also confirmed that a termination codon exists in the 3'-terminus of GPA/WT DNA without intervening

sequences.

The recombinant DNA pBlgGPA/WT was introduced into a cell line C127 (ATCC CRL-1616), derived from a mouse, by using a lipofectin® reagent commercialized by Life Technologies, Inc., Gaithersburg, U.S.A., according to the attached protocol. The transformants with the recombinant DNA were selected based on the lack of proliferation-regulatory ability, i.e., focus-forming ability, as a first selection. The cells around those containing foci were collected using sterilized filter papers and subjected to a conventional limiting dilution method to form single cells which were then selected depending on the productivity of L-asparaginase, as final selection. Thus, a transformant, "C-GPA/WT", was obtained.

Example A-2(b)

Production of polypeptide

The transformant C-GPA/WT was inoculated into a well of "3046", a plastic multiwell plate with 6 wells, 3.5 cm in diameter, commercialized by Becton Dickinson Labware, New Jersey, U.S.A., with DME medium containing 10 v/v % bovine fetal serum, and cultured to be confluent as a seed culture. Some of the cells, scraped by treatment with trypsin, were inoculated as seed cells into each of the multiwell plates which were charged with the fresh preparation of the same medium and cultured. After repeating manipulations similarly as in the above and with scale up to increase the cell number, the cells were subjected to a conventional continuous culture using 50 of 150 cm² culture flasks. The resulting culture supernatants of a volume of 100 l was collected and treated with similar methods for treating the supernatant from the cell-disruptants in Example A-1(b): salting out with ammonium sulfate, the chromatography of the solution of the precipitates using Q SEPHAROSE FF COLUMN, the chromatography of the eluted fractions using L-ASPARAGINE AGAROSE, and the chromatography of the eluted fractions using HILOAD SUPERDEX 200 COLUMN. Consequently, a purified polypeptide with a purity of 90 % or more was obtained in a yield of about one µg/ml-culture.

Example A-2(c)

Physicochemical property of polypeptide

By testing similarly as in Example A-1(c), it was confirmed that the purified polypeptide thus obtained had equivalent physicochemical properties with the that obtained in Example A-1(b).

Example A-3(a)

Preparation of transformant

PCRs were performed under the same conditions in Example A-1(a) except for the template and the sense- and anti-sense-primers. The DNA thus obtained were treated similarly as in Example A-1(a) to prepare recombinant DNAs, "pKGPA/D364stp", "pKHA/MUT1", "pKHA/MUT2", "pKHA/MUT3" and "pKHA/MUT5". Table 5 summarizes template DNAs and nucleotide sequences of a sense- and anti-sense-primers which were used to prepare the each recombinant DNAs. By sequencing similarly as in Example A-1(a), the structures of these recombinant DNAs were confirmed as shown in FIGs. 5 to 9.

Table 5

Recombinant DNA	Template DNA	Nucleotide sequences of sense (upper line) and anti-sense (lower line) primers *
pKGPA/D364stp	pCGPA/D364stp	5'-GCGAATTTCATGGCGCGCATCA-3' 5'-GCAAGCTTTCATGCCGTGGGCAGTGT-3'
pKHA/MUT1	pCHA/MUT1	5'-GCGAATTTCATGGCGCGGGTG-3' 5'-GCAAGCTTTCACACCGAGGGTGGCGT-3'
pKHA/MUT2	pCHA/MUT2	the same as used for pKHA/MUT1 preparation the same as used for pKHA/MUT1 preparation
pKHA/MUT3	pCHA/MUT3	the same as used for pKHA/MUT1 preparation the same as used for pKHA/MUT1 preparation
pKHA/MUT5	pCHA/MUT5	the same as used for pKHA/MUT1 preparation the same as used for pKHA/MUT1 preparation

*) Italics in the upper line in each column mean the 5'-terminal nucleotide sequence of a DNA encoding L-asparaginase, and those in the lower line mean the complementary sequence to the 3'-terminus of the DNA, wherein the L-asparaginase originates from a guinea pig or human.

The recombinant DNAs were treated according to the methods as in Example A-1(a) to obtain transformants, "J-GPA/D364stp", "J-HA/MUT1", "J-HA/MUT2", "J-HA/MUT3" and "J-HA/MUTS".

Example A-3(b)

Production of polypeptide

The transformants obtained in Example A-3(a) were treated according to the methods similarly as in Example A-1(b): cultivation, disrupting the resulting cells, the precipitations of the cell-disruptants with ammonium sulfate, the chromatography of the precipitate solutions using Q SEPHAROSE FF COLUMN, and the chromatography of the eluted fractions using L-ASPARAGINE AGAROSE in that order. The eluted fractions thus obtained were concentrated using membranes similarly as in Example A-1(b) followed by subjecting the chromatography using HILOAD SUPERDEX 200 COLUMN to collect the eluted fractions with a molecular weight of about 140 kDa. Each system yielded the purified polypeptide with a purity of 90 % or more in a yield of about 0.1 mg/ml-culture. These purified polypeptides were analyzed by the methods as in Example A-1(c) to examine their physicochemical properties. Table 6 shows the results combined with those in Example A-1(c).

Table 6

Transformant, producing the polypeptide	Molecular weight (kDa) *1	Molecular weight (kDa) *2	L-asparaginase activity
J-GPA/WT	about 300	about 50 ± 10	+
J-GPA/D364stp	about 140	about 40	+
J-HA/MUT1	about 140	about 40	+
J-HA/MUT2	about 140	about 40	+
J-HA/MUT3	about 140	about 40	+
J-HA/MUT5	about 140	about 40	+

Note) The symbols "*1" and "*2" mean that the value was determined by gel filtration, and the value was determined by SDS-PAGE, respectively.

Table 6 indicates that all of the present polypeptides, expressed in *Escherichia coli* and purified, expressed an L-asparaginase activity. Furthermore, table 6 indicates that the polypeptides formed tetramers.

Example A-4(a)

Preparation of transformants

PCRs were performed under the same conditions in Example A-1(a) except for the template and the sense- and anti-sense-primers. DNAs thus obtained were ligated with the same linkers as used in Example A-2(a) under the same conditions as in Example A-2(a) to obtain recombinant DNAs, "pBtgPA/D364stp", "pBtgHA/MUT1", "pBtgHA/MUT2", "pBtgHA/MUT3" and "pBtgHA/MUT5". Table 7 summarizes template DNAs and nucleotide sequences of sense- and anti-sense-primers which were used to prepare the each recombinant DNAs. By sequencing similarly as in Example A-1(a), the structures of these recombinant DNAs were confirmed as shown in FIGs.10 to 14.

Table 7

Recombinant DNA	Template DNA	Nucleotide sequences of sense (upper line) and anti-sense (lower line) primers *
pBIGPA/D364stp	PCGPA/D364stp	5'-GTGAATTTCGGAGGTTTCAGATGGCGCGCATCA-3' 5'-CTGCGGCGGCTCATGCCCTGGGCAGTG-3'
pBIGHA/MUT1	pCHA/MUT1	5'-CTGAATTTCGGAGGTTTCAGATGGCGCGCGTG-3' 5'-CTGCGGCGGCTCACACCGAGGTGGCG-3'
pBIGHA/MUT2	pCHA/MUT2	the same as used for pBIGHA/MUT1 preparation the same as used for pBIGHA/MUT1 preparation
pBIGHA/MUT3	pCHA/MUT3	the same as used for pBIGHA/MUT1 preparation the same as used for pBIGHA/MUT1 preparation
pBIGHA/MUT5	pCHA/MUT5	the same as used for pBIGHA/MUT1 preparation the same as used for pBIGHA/MUT1 preparation

Note) *: Italics in the upper line in each column mean the 5'-terminal nucleotide sequence of a DNA encoding L-asparaginase, and those in the lower line mean the complementary sequence to the 3'-terminus of the DNA, wherein the L-asparaginase originates from a guinea pig or human.

The recombinant DNAs thus obtained were treated similarly as in Example A-2(a) to obtain transformants, "C-GPA/D364stp", "C-HA/MUT1", "C-HA/MUT2", "C-HA/MUT3" and "C-HA/MUTS".

Example A-4(b)

Production of polypeptide

The transformants obtained in Example A-4(a) were cultured according to the methods as in Example A-2(b), and the resulting culture supernatants were treated with similar methods for treating the supernatants from the cell-disruptants in Example A-1(b): the precipitations of culture supernatants with ammonium sulfate, the chromatography of the precipitate solutions using Q SEPHAROSE FF COLUMN, and the chromatography of the eluted fractions using L-ASPARAGINE AGAROSE in that order. The eluted fractions thus obtained were concentrated using membranes similarly as in Example A-1(b) followed by subjecting the chromatography using HILOAD SUPERDEX 200 COLUMN to collect the eluted fractions with a molecular weights of about 140 kDa. Each of these systems yielded the purified polypeptide with a purity of 90 % or more in a yield of about one µg/ml-culture. These purified polypeptides were analyzed by the methods as in Example A-1(c) to examine their physicochemical properties. Table 8 shows the results combined with those in Example A-3.

Table 8

The polypeptide- producing transformant	Molecular weight (kDa) *1	Molecular weight (kDa) *2	L-asparaginase activity
J-GPA/WT	about 300	about 50 ± 10	+
J-GPA/D364stp	about 140	about 40	+
J-HA/MUT1	about 140	about 40	+
J-HA/MUT2	about 140	about 40	+
J-HA/MUT3	about 140	about 40	+
J-HA/MUT5	about 140	about 40	+

Note) The symbols "*1" and "*2" mean that the value was determined by gel filtration,
and the value was determined by SDS-PAGE, respectively.

Table 8 indicates that all of the present polypeptides, expressed in mammalian cells and purified, expressed an L-asparaginase activity. Furthermore, table 8 indicates the polypeptides formed tetramers.

As shown in above Example A, each of the polypeptides according to the present invention expresses an L-asparaginase activity. Therefore, the present agent for susceptible diseases hydrolyze L-asparagine in patients to exert therapeutic and preventive effects on L-asparaginase-susceptible diseases when administered to human. The wording "susceptible diseases" as referred in the present specification means diseases in general which are caused by the existence of tumor cells dependent on L-asparagine: For example, leukemias such as acute leukemia, an acute transformation of chronic leukemia and T-lymphocytic leukemia, and malignant tumors such as Hodgkin's diseases and non-Hodgkin's diseases. The present agent for susceptible diseases possesses thus the uses as anti-tumor agents for treating and/or preventing such susceptible diseases as above. Although it varies dependently on the types of agents used for such purposes and susceptible diseases to be treated, the present agent is generally processed into an agent in the form of a liquid, a paste or a solid which contains the polypeptides in an amount of 0.000001-100 w/w %, preferably, 0.0001-100 w/w %, on a dry solid basis.

The present agent can be used intact or processed into compositions by mixing with one or more selected from the group consisting of physiologically-acceptable carriers, excipients, solvents, buffers and stabilizers, and further, if necessary, other biologically-active substances and other agents. For example, "Iyakuhin-Tenkabutsu-Jiten (The Dictionary of Pharmaceutical Excipients)" (1994), edited by Japan Pharmaceutical Excipients Council, Tokyo, Japan, published by Yakujinippo LTD., Tokyo, Japan and "Iyakuhin-Tenkabutsu-Jiten-Tsuiho 1995 (Supplement for The Dictionary of Pharmaceutical Excipients)" (1995), edited by Japan Pharmaceutical Excipients Council, Tokyo, Japan, published by Yakujinippo LTD., Tokyo, Japan, mention the embodiments of such carriers, excipients, solvents, buffers and stabilizers. Examples of such other biologically-active substances and other agents include interferon- α , interferon- β , interferon- γ , interleukin 1, interleukin 2, interleukin 3, TNF- α , TNF- β , GM-CSF, carboquone, cyclophosphamide, aclarubicin, thiotepea, busulfan, ancitabine, cytarabine, fluorouracil, 5-fluoro-1-(tetrahydro-2-furyl)uracil, methotrexate, actinomycin D, chromomycin A3, daunorubicin, doxorubicin, bleomycin, mercaptopurine, prednisolone, mitomycin C, vincristine, vinblastine, radio gold colloidal, Krestin®, picibanil, lentinan and Maruyama vaccine.

The present agent for susceptible diseases includes those in a unit dose form which means a physically separated and formed medicament suitable for administration, and contains the polypeptides in a daily dose or in a dose from 1/40 to several folds (up to 4 folds) of the daily dose. Examples of such medicaments are injections, liquids, powders, granules, tablets, capsules, sublinguals, ophthalmic solutions, nasal drops and suppositories.

The present agent can be administered to patients orally or parenterally. In both administrations, the agent exerts a satisfactory effect in the treatment and/or the prevention for the susceptible diseases. Although it varies dependently on the types of susceptible diseases and their symptoms, the agent can be orally administered to patients or parenterally administered to patients' intradermal tissues, subcutaneous tissues, muscles, and veins at a dose as amounts of the polypeptides in the range of about 0.1 μ g - 500 mg/shot, preferably, about 0.1-100 mg/shot, 1-4 times/day or 1-7 times/week, for one day to one year. The present agent for susceptible diseases further includes the forms by applying gene therapy. When a transformant into which the DNAs encoding the polypeptides of this invention are introduced are administered to patients to express in them, they exert equivalent effects as above administrations. For example, "Jikken-Igaku Bessatsu, Bio-manual Up Series, Idenshi-Chiryō-No-Kisogijutsu (Basic Techniques for Gene Therapy)" (1996), edited by Takashi SHIMADA, Izumi SAITO and Takaya OZAWA, published by Yodosha, Tokyo, Japan, details the general procedures for the gene therapy.

The biological activities and acute toxicity of the present polypeptides are explained based on Experiment 3 and 4 below, respectively.

Experiment 3

Biological activity

Experiment 3-1

Antitumor effect *in vitro*

A human histocytic lymphoma cell line U937 (ATCC CRL-1593), and a cell line Molt4 (ATCC CRL-1582), derived from human T lymphoblasts, were subcultured in RPMI 1640 medium containing 10 v/v % bovine fetal serum. The cells collected by centrifugation from each subculturing system in logarithmic phase were suspended in the same medium to give a concentration of 2×10^5 cells/ml. Every one ml of the each cell suspension was charged into each of 13 wells of multiwell plates with 24 wells, "3047", commercialized by Becton Dickinson Labware, New Jersey, U.S.A. After each of dilutions of 12 types of the purified polypeptides prepared in Example A-1 to A-4 with PBS was further charged into the each well, the cells were cultured at 37°C for 72 hours in a 5 v/v % CO₂ incubator. The final concen-

tration of each of the purified polypeptides was one unit/ml as an L-asparaginase activity. As a control, after charged with equivalent volume of PBS, the cells were cultured correspondingly. The cells were collected after the cultivation to stain cells died with trypan blue. Cell survival ratio in each systems with the purified polypeptides was compared with that in the control. All of the cell survival ratios with the purified polypeptides were significantly lower than that in the control. These results indicate that all of the present polypeptides, obtained in Examples A-1 to A-4, have cytotoxicity to U937 and Molt4.

Experiment 3-2

Antitumor effect *in vivo*

For model mice were used C3H mice wherein a mouse lymphoma cell line 6C3HED, registered in Cell Resource Center for Biomedical Research, Institute of Development Aging and Cancer, Tohoku University, Sendai, Japan, was transplanted with passages by subcutaneous injections at their sides in a range of 1×10^7 cells/body every 8 days in usual manner. To the model mice were administered the purified polypeptides obtained in Example A-1 to A-4 in the range of 400 unit/body by venoclyses every day from fourth to seventh days after transplanted with the cells. Dimensions of the tumors were observed with naked eyes on fourth and eighth day after the transplantations. The purified polypeptides were administered after diluted with 0.15 M NaCl and filtrated with membrane filters, 0.45 μ m in pore size, commercialized by Millipore Corp., Bedford, U.S.A. As a control, 0.15 M NaCl was treated correspondingly. While significant enlargements of the tumors were observed in the control, significant involutions or disappearances of the tumors were observed in mice administered with the polypeptides. These results indicates that all of the present polypeptides, obtained in Examples A-1 to A-4, are able to cure the tumors of model mice.

Experiment 4

Acute toxicity

The purified polypeptides obtained in Examples A-1 to A-4 were separately administered to 8-week-old mice percutaneously, perorally or intraperitoneally according to conventional manner. The LD₅₀ of all the polypeptides was about 100 mg/kg or higher independently of the administration routes. These results evidenced that the present polypeptides could be safely incorporated into pharmaceuticals for administering human.

The following examples explain the present agent for susceptible diseases.

Example B-1

Solution

The purified polypeptides obtained in Examples A-1 to A-4 were separately dissolved to give a concentration of 0.1 mg/ml in physiological saline containing one w/v % human serum albumin as a stabilizer, and sterilized with membrane filters according to conventional manner to obtain solutions.

All of the products have satisfactory stabilities and can be used as injections, ophthalmic solutions, collunarium in the treatment and/or the prevention of susceptible diseases including a malignant tumor, acute leukemia, malignant lymphoma, an acute transformation of chronic leukemia, T-lymphocytic leukemia.

Example B-2

Solution

The purified polypeptides obtained in Examples A-1 to A-4 were separately dissolved to give a concentration of 0.1 mg/ml in physiological saline containing one w/v % glycerol as a stabilizer, and sterilized with membrane filters according to conventional manner to obtain solutions.

All of the products have satisfactory stabilities and can be used as injections, ophthalmic solutions, collunarium for the treatment and/or the prevention of susceptible diseases including a malignant tumor, acute leukemia, malignant lymphoma, an acute transformation of chronic leukemia and T-lymphocytic leukemia.

Example B-3Dry injection

5 The purified polypeptides obtained in Examples A-1 to A-4 were separately dissolved to give a concentration of 50 mg/ml in physiological saline containing one w/v % purified gelatin as a stabilizer, and the solutions were sterilized with membrane filters according to conventional manner. One ml aliquots of the sterilized solutions were distributed to vials, lyophilized and cap sealed.

10 All of the products have satisfactory stabilities and can be used as dry injections for the treatment and/or the prevention of susceptible diseases including a malignant tumor, acute leukemia, malignant lymphoma, an acute transformation of chronic leukemia and T-lymphocytic leukemia.

Example B-4Ointment

15 "HI-BIS-WAKO 104", a carboxyvinyl polymer commercialized by Wako Pure Chemicals, Tokyo, Japan, and a purified trehalose were dissolved in sterilized distilled water to give concentrations of 1.4 w/w % and 2.0 w/w %, respectively, and the purified polypeptides obtained in Examples A-1 to A-4 were separately mixed to homogeneity in the solutions followed by adjusting the pH of the resulting solutions to pH 7.2 to obtain pastes containing about one mg/g of the polypeptides.

20 All of the products have satisfactory spreadabilities and stabilities, and can be used as ointments for treating and/or preventing susceptible diseases including a malignant tumor, acute leukemia, malignant lymphoma, an acute transformation of chronic leukemia and T-lymphocytic leukemia.

Example B-5Tablet

30 Any one of the purified polypeptides obtained in Examples A-1 to A-4 and LUMIN, i.e. [bis-4-(1-ethylquinoline)][γ -4'-(1-ethylquinoline) pentamethionine cyanine, as a cell activator were mixed to homogeneity with "FINETOSE®" an hydrous crystalline α -maltose commercialized by Hayashibara Co., Ltd., Okayama, Japan, and the mixtures were tableted by tableting machine to obtain tablets, about 200 mg weight each, containing the polypeptide and the LUMIN, about 5 mg each.

35 All of the products have satisfactory swallowing abilities, stabilities and cell activating activities, and can be used for treating and/or preventing susceptible diseases including a malignant tumor, acute leukemia, malignant lymphoma, an acute transformation of chronic leukemia and T-lymphocytic leukemia.

40 The present invention is based on the findings of polypeptides which originate from mammal, having L-asparaginase activity. The polypeptides are substances which have revealed amino acid sequences totally, and stable activities to hydrolyze L-asparagine. Therefore, the polypeptides exert satisfactory effects in the treatment and/or the prevention for diseases caused by tumor cells dependent on L-asparagine.

The polypeptides originate from mammal, so that they have low antigenicities to human and don't cause serious side effects even when administered in large amounts or continuously. Therefore, the polypeptides have the advantage that they can exert desired effects without restricted controls on patients' sensitivities.

45 The polypeptides thus valuable can be produced in desired amounts using the present DNAs encoding them.

Thus, the present invention is a significant invention which has a remarkable effect and gives a great contribution to this field.

50 While there has been described what is at present considered to be the preferred embodiments of the present invention, it will be understood the various modifications may be made therein, and it is intended to cover in the appended claims all such modifications as fall within the true spirits and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
KENKYUJO

(ii) TITLE OF INVENTION: POLYPEPTIDES HAVING L-ASPARAGINASE ACTIVITY

(iii) NUMBER OF SEQUENCES: 18

(iv) ADDRESS:

(A) ADDRESSEE: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
KENKYUJO

(B) STREET: 2-3, 1-CHOME, SHIMOISHII

(C) CITY: OKAYAMA

(E) COUNTRY: JAPAN

(F) POSTAL CODE (ZIP): 700

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: Word Perfect Version 5.1

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 168,172/96

(B) FILING DATE: June 7, 1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Thr Gly Gly Thr

1

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

His Gly Thr Asp Thr
1 5

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Cys Leu Xaa Gly
1 5

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Arg	Ala	Ser	Gly	Ser	Glu	Arg	His	Leu	Leu	Leu	Ile	Tyr	Thr
1				5					10					15	
Gly	Gly	Thr	Leu	Gly	Met	Gln	Ser	Lys	Gly	Gly	Val	Leu	Val	Pro	Gly
			20					25					30		
Pro	Gly	Leu	Val	Thr	Leu	Leu	Arg	Thr	Leu	Pro	Met	Phe	His	Asp	Lys
		35					40					45			
Glu	Phe	Ala	Gln	Ala	Gln	Gly	Leu	Pro	Asp	His	Ala	Leu	Ala	Leu	Pro
	50					55					60				
Pro	Ala	Ser	His	Gly	Pro	Arg	Val	Leu	Tyr	Thr	Val	Leu	Glu	Cys	Gln
65					70					75				80	
Pro	Leu	Leu	Asp	Ser	Ser	Asp	Met	Thr	Ile	Asp	Asp	Trp	Ile	Arg	Ile
			85						90					95	
Ala	Lys	Ile	Ile	Glu	Arg	His	Tyr	Glu	Gln	Tyr	Gln	Gly	Phe	Val	Val
			100					105					110		
Ile	His	Gly	Thr	Asp	Thr	Met	Ala	Phe	Gly	Ala	Ser	Met	Leu	Ser	Phe
		115				120						125			
Met	Leu	Glu	Asn	Leu	His	Lys	Pro	Val	Ile	Leu	Thr	Gly	Ala	Gln	Val
	130					135					140				
Pro	Ile	Arg	Val	Leu	Trp	Asn	Asp	Ala	Arg	Glu	Asn	Leu	Leu	Gly	Ala
145					150					155				160	
Leu	Leu	Val	Ala	Gly	Gln	Tyr	Ile	Ile	Pro	Glu	Val	Cys	Leu	Phe	Met
			165						170					175	
Asn	Ser	Gln	Leu	Phe	Arg	Gly	Asn	Arg	Val	Thr	Lys	Val	Asp	Ser	Gln
			180					185					190		
Lys	Phe	Glu	Ala	Phe	Cys	Ser	Pro	Asn	Leu	Ser	Pro	Leu	Ala	Thr	Val
		195					200					205			
Gly	Ala	Asp	Val	Thr	Ile	Ala	Trp	Asp	Leu	Val	Arg	Lys	Val	Asn	Trp
	210					215					220				
Lys	Asp	Pro	Leu	Val	Val	His	Ser	Asn	Met	Glu	His	Asp	Val	Ala	Leu
225					230					235				240	
Leu	Arg	Leu	Tyr	Pro	Gly	Ile	Pro	Ala	Ser	Leu	Val	Arg	Ala	Phe	Leu

5 Gln Pro Pro Leu Lys Gly Val Val Leu Glu Thr Phe Gly Ser Gly Asn
 245 250 255
 Gly Pro Ser Lys Pro Asp Leu Leu Glu Leu Arg Ala Ala Gln
 260 265 270
 Arg Gly Leu Ile Met Val Asn Cys Ser Gln Cys Leu Arg Gly Ser Val
 275 280 285
 Thr Pro Gly Tyr Ala Thr Ser Leu Ala Gly Ala Asn Ile Val Ser Gly
 290 295 300 305
 10 Leu Asp Met Thr Ser Glu Ala Ala Leu Ala Lys Leu Ser Tyr Val Leu
 310 315 320
 Gly Leu Pro Glu Leu Ser Leu Glu Arg Arg Gln Glu Leu Leu Ala Lys
 325 330 335
 15 Asp Leu Arg Gly Glu Met Thr Leu Pro Thr Ala
 340 345 350 355 360 363

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 565 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Arg Ala Ser Gly Ser Glu Arg His Leu Leu Leu Ile Tyr Thr
 1 5 10 15
 Gly Gly Thr Leu Gly Met Gln Ser Lys Gly Gly Val Leu Val Pro Gly
 20 25 30
 30 Pro Gly Leu Val Thr Leu Leu Arg Thr Leu Pro Met Phe His Asp Lys
 35 40 45
 Glu Phe Ala Gln Ala Gln Gly Leu Pro Asp His Ala Leu Ala Leu Pro
 50 55 60
 Pro Ala Ser His Gly Pro Arg Val Leu Tyr Thr Val Leu Glu Cys Gln
 65 70 75 80
 35 Pro Leu Leu Asp Ser Ser Asp Met Thr Ile Asp Asp Trp Ile Arg Ile
 85 90 95
 Ala Lys Ile Ile Glu Arg His Tyr Glu Gln Tyr Gln Gly Phe Val Val
 100 105 110
 40 Ile His Gly Thr Asp Thr Met Ala Phe Gly Ala Ser Met Leu Ser Phe
 115 120 125
 Met Leu Glu Asn Leu His Lys Pro Val Ile Leu Thr Gly Ala Gln Val
 130 135 140
 Pro Ile Arg Val Leu Trp Asn Asp Ala Arg Glu Asn Leu Leu Gly Ala
 145 150 155 160
 45 Leu Leu Val Ala Gly Gln Tyr Ile Ile Pro Glu Val Cys Leu Phe Met
 165 170 175
 Asn Ser Gln Leu Phe Arg Gly Asn Arg Val Thr Lys Val Asp Ser Gln
 180 185 190
 Lys Phe Glu Ala Phe Cys Ser Pro Asn Leu Ser Pro Leu Ala Thr Val
 195 200 205
 50 Gly Ala Asp Val Thr Ile Ala Trp Asp Leu Val Arg Lys Val Asn Trp
 210 215 220
 Lys Asp Pro Leu Val Val His Ser Asn Met Glu His Asp Val Ala Leu
 225 230 235 240
 55 Leu Arg Leu Tyr Pro Gly Ile Pro Ala Ser Leu Val Arg Ala Phe Leu

5 245 250 255
 Gln Pro Pro Leu Lys Gly Val Val Leu Glu Thr Phe Gly Ser Gly Asn
 260 265 270
 Gly Pro Ser Lys Pro Asp Leu Leu Gln Glu Leu Arg Ala Ala Ala Gln
 275 280 285
 Arg Gly Leu Ile Met Val Asn Cys Ser Gln Cys Leu Arg Gly Ser Val
 290 295 300
 10 Thr Pro Gly Tyr Ala Thr Ser Leu Ala Gly Ala Asn Ile Val Ser Gly
 305 310 315 320
 Leu Asp Met Thr Ser Glu Ala Ala Leu Ala Lys Leu Ser Tyr Val Leu
 325 330 335
 Gly Leu Pro Glu Leu Ser Leu Glu Arg Arg Gln Glu Leu Leu Ala Lys
 340 345 350
 15 Asp Leu Arg Gly Glu Met Thr Leu Pro Thr Ala Asp Leu His Gln Ser
 355 360 365
 Ser Pro Pro Gly Ser Thr Leu Gly Gln Gly Val Ala Arg Leu Phe Ser
 370 375 380
 Leu Phe Gly Cys Gln Glu Asp Ser Val Gln Asp Ala Val Met Pro
 385 390 395 400
 20 Ser Leu Ala Leu Ala Leu Ala His Ala Gly Glu Leu Glu Ala Leu Gln
 405 410 415
 Ala Leu Met Glu Leu Gly Ser Asp Leu Arg Leu Lys Asp Ser Asn Gly
 420 425 430
 Gln Thr Leu Leu His Val Ala Ala Arg Asn Gly Arg Asp Gly Val Val
 435 440 445
 25 Thr Met Leu Leu His Arg Gly Met Asp Val Asn Ala Arg Asp Arg Asp
 450 455 460
 Gly Leu Ser Pro Leu Leu Leu Ala Val Gln Gly Arg His Arg Glu Cys
 465 470 475 480
 30 Ile Arg Leu Leu Arg Lys Ala Gly Ala Cys Leu Ser Pro Gln Asp Leu
 485 490 495
 Lys Asp Ala Gly Thr Glu Leu Cys Arg Leu Ala Ser Arg Ala Asp Met
 500 505 510
 Glu Gly Leu Gln Ala Trp Gly Gln Ala Gly Ala Asp Leu Gln Gln Pro
 515 520 525
 35 Gly Tyr Asp Gly Arg Ser Ala Leu Cys Val Ala Glu Ala Ala Gly Asn
 530 535 540
 Gln Glu Val Leu Ala Leu Leu Arg Asn Leu Ala Leu Val Gly Pro Glu
 545 550 555 560
 Val Pro Pro Ala Ile
 565

(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

50 Met Ala Arg Ala Val Gly Pro Glu Arg Arg Leu Leu Ala Val Tyr Thr
 1 5 10 15
 Gly Gly Thr Ile Gly Met Arg Ser Glu Leu Gly Val Leu Val Pro Gly
 20 25 30
 Thr Gly Leu Ala Ala Ile Leu Arg Thr Leu Pro Met Phe His Asp Glu

5 35 40 45
 Glu His Ala Arg Ala Arg Gly Leu Ser Glu Asp Thr Leu Val Leu Pro
 50 55 60
 Pro Asp Ser Arg Asn Gln Arg Ile Leu Tyr Thr Val Leu Glu Cys Gln
 65 70 75 80
 Pro Leu Phe Asp Ser Ser Asp Met Thr Ile Ala Glu Trp Val Arg Val
 85 90 95
 10 Ala Gln Thr Ile Lys Arg His Tyr Glu Gln Tyr His Gly Phe Val Val
 100 105 110
 Ile His Gly Thr Asp Thr Met Ala Phe Ala Ala Ser Met Leu Ser Phe
 115 120 125
 Met Leu Glu Asn Leu Gln Lys Thr Val Ile Leu Thr Gly Ala Gln Val
 130 135 140
 15 Pro Ile His Ala Leu Trp Ser Asp Gly Arg Glu Asn Leu Leu Gly Ala
 145 150 155 160
 Leu Leu Met Ala Gly Gln Tyr Val Ile Pro Glu Val Cys Leu Phe Phe
 165 170 175
 20 Gln Asn Gln Leu Phe Arg Gly Asn Arg Ala Thr Lys Val Asp Ala Arg
 180 185 190
 Arg Phe Ala Ala Phe Cys Ser Pro Asn Leu Leu Pro Leu Ala Thr Val
 195 200 205
 Gly Ala Asp Ile Thr Ile Asn Arg Glu Leu Val Arg Lys Val Asp Gly
 210 215 220
 25 Lys Ala Gly Leu Val Val His Ser Ser Met Glu Gln Asp Val Gly Leu
 225 230 235 240
 Leu Arg Leu Tyr Pro Gly Ile Pro Ala Ala Leu Val Arg Ala Phe Leu
 245 250 255
 Gln Pro Pro Leu Lys Gly Val Val Met Glu Thr Phe Gly Ser Gly Asn
 260 265 270
 30 Gly Pro Thr Lys Pro Asp Leu Leu Gln Glu Leu Arg Val Ala Thr Glu
 275 280 285
 Arg Gly Leu Val Ile Val Asn Cys Thr Gln Cys Leu Arg Gly Ala Val
 290 295 300
 35 Thr Thr Asp Tyr Ala Ala Gly Met Ala Met Ala Gly Ala Asn Val Ile
 305 310 315 320
 Ser Gly Phe Asp Met Thr Ser Glu Ala Ala Leu Ala Lys Leu Ser Tyr
 325 330 335
 Val Leu Gly Gln Pro Gly Leu Ser Leu Asp Val Arg Lys Glu Leu Leu
 340 345 350
 40 Thr Lys Asp Leu Arg Gly Glu Met Thr Pro Pro Ser Val
 355 360 365

(8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:365 amino acids

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULAR TYPE:peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:7:

Met Ala Arg Ala Val Gly Pro Glu Arg Arg Leu Leu Ala Val Tyr Thr
 1 5 10 15
 Gly Gly Thr Ile Gly Met Arg Ser Glu Leu Gly Val Leu Val Pro Gly
 20 25 30
 55 Thr Gly Leu Ala Ala Ile Leu Arg Thr Leu Pro Met Phe His Asp Glu

		35		40		45											
	Glu	His	Ala	Arg	Ala	Arg	Gly	Leu	Ser	Glu	Asp	Thr	Leu	Val	Leu	Pro	
5		50					55					60					
	Pro	Asp	Ser	Arg	Asn	Gln	Arg	Ile	Leu	Tyr	Thr	Val	Leu	Glu	Cys	Gln	
	65					70					75					80	
	Pro	Leu	Phe	Asp	Ser	Ser	Asp	Met	Thr	Ile	Ala	Glu	Trp	Val	Arg	Val	
					85						90				95		
10	Ala	Gln	Thr	Ile	Lys	Arg	His	Tyr	Glu	Gln	Tyr	His	Gly	Phe	Val	Val	
				100					105					110			
	Ile	His	Gly	Thr	Asp	Thr	Met	Ala	Phe	Ala	Ala	Ser	Met	Leu	Ser	Phe	
			115					120					125				
	Met	Leu	Glu	Asn	Leu	Gln	Lys	Thr	Val	Ile	Leu	Thr	Gly	Ala	Gln	Val	
		130					135					140					
15	Pro	Ile	His	Ala	Leu	Trp	Ser	Asp	Gly	Arg	Glu	Asn	Leu	Leu	Gly	Ala	
	145					150					155					160	
	Leu	Leu	Met	Ala	Gly	Gln	Tyr	Val	Ile	Pro	Glu	Val	Cys	Leu	Phe	Phe	
					165					170					175		
	Gln	Asn	Gln	Leu	Phe	Arg	Gly	Asn	Arg	Ala	Thr	Lys	Val	Asp	Ala	Arg	
				180					185					190			
20	Arg	Phe	Ala	Ala	Phe	Cys	Ser	Pro	Asn	Leu	Leu	Pro	Leu	Ala	Thr	Val	
			195					200					205				
	Gly	Ala	Asp	Ile	Thr	Ile	Asn	Arg	Glu	Leu	Val	Arg	Lys	Val	Asp	Gly	
		210					215					220					
25	Lys	Ala	Gly	Leu	Val	Val	His	Ser	Ser	Met	Glu	Gln	Asp	Val	Gly	Leu	
	225					230					235					240	
	Leu	Arg	Leu	Tyr	Pro	Gly	Ile	Pro	Ala	Ala	Leu	Val	Arg	Ala	Phe	Leu	
					245					250					255		
	Gln	Pro	Pro	Leu	Lys	Gly	Val	Val	Met	Glu	Thr	Phe	Gly	Ser	Gly	Asn	
				260					265					270			
30	Gly	Pro	Thr	Lys	Pro	Asp	Leu	Leu	Gln	Glu	Leu	Arg	Val	Ala	Thr	Glu	
			275					280					285				
	Arg	Gly	Leu	Val	Ile	Val	Asn	Cys	Thr	Gln	Cys	Leu	Arg	Gly	Ala	Val	
		290					295					300					
	Thr	Thr	Asp	Tyr	Ala	Ala	Gly	Met	Ala	Met	Ala	Gly	Ala	Gly	Val	Ile	
	305					310					315					320	
35	Ser	Gly	Phe	Asp	Met	Thr	Ser	Glu	Ala	Ala	Leu	Ala	Lys	Leu	Ser	Tyr	
					325					330					335		
	Val	Leu	Gly	Gln	Pro	Gly	Leu	Ser	Leu	Asp	Val	Arg	Lys	Glu	Leu	Leu	
				340					345					350			
40	Thr	Lys	Asp	Leu	Arg	Gly	Glu	Met	Thr	Pro	Pro	Ser	Val				
			355				360						365				

(9) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	Met	Ala	Arg	Ala	Val	Gly	Pro	Glu	Arg	Arg	Leu	Leu	Ala	Val	Tyr	Thr
	1				5					10					15	
	Gly	Gly	Thr	Ile	Gly	Met	Arg	Ser	Glu	Leu	Gly	Val	Leu	Val	Pro	Gly
				20					25				30			
55	Thr	Gly	Leu	Ala	Ala	Ile	Leu	Arg	Thr	Leu	Pro	Met	Phe	His	Asp	Glu

5 35 40 45
 Glu His Ala Arg Ala Arg Gly Leu Ser Glu Asp Thr Leu Val Leu Pro
 50 55 60
 Pro Asp Ser Arg Asn Gln Arg Ile Leu Tyr Thr Val Leu Glu Cys Gln
 65 70 75 80
 Pro Leu Phe Asp Ser Ser Asp Met Thr Ile Ala Glu Trp Val Arg Val
 85 90 95
 10 Ala Gln Thr Ile Lys Arg His Tyr Glu Gln Tyr His Gly Phe Val Val
 100 105 110
 Ile His Gly Thr Asp Thr Met Ala Phe Ala Ala Ser Met Leu Ser Phe
 115 120 125
 Met Leu Glu Asn Leu Gln Lys Thr Val Ile Leu Thr Gly Ala Gln Val
 130 135 140
 15 Pro Ile His Ala Leu Trp Ser Asp Gly Arg Glu Asn Leu Leu Gly Ala
 145 150 155 160
 Leu Leu Met Ala Gly Gln Tyr Val Ile Pro Glu Val Cys Leu Phe Phe
 165 170 175
 20 Gln Asn Gln Leu Phe Arg Gly Asn Arg Ala Thr Lys Val Asp Ala Arg
 180 185 190
 Arg Phe Ala Ala Phe Cys Ser Pro Asn Leu Leu Pro Leu Ala Thr Val
 195 200 205
 Gly Ala Asp Ile Thr Ile Asn Arg Glu Leu Val Arg Lys Val Asp Gly
 210 215 220
 25 Lys Ala Gly Leu Val Val His Ser Ser Met Glu Gln Asp Val Gly Leu
 225 230 235 240
 Leu Arg Leu Tyr Pro Gly Ile Pro Ala Ala Leu Val Arg Ala Phe Leu
 245 250 255
 Gln Pro Pro Leu Lys Gly Val Val Met Glu Thr Phe Gly Ser Gly Asn
 260 265 270
 30 Gly Pro Thr Lys Pro Asp Leu Leu Gln Glu Leu Arg Val Ala Thr Glu
 275 280 285
 Arg Gly Leu Val Ile Val Asn Cys Thr Gln Cys Leu Gln Gly Ala Val
 290 295 300
 35 Thr Thr Asp Tyr Ala Ala Gly Met Ala Met Ala Gly Ala Asn Val Ile
 305 310 315 320
 Ser Gly Phe Asp Met Thr Ser Glu Ala Ala Leu Ala Lys Leu Ser Tyr
 325 330 335
 Val Leu Gly Gln Pro Gly Leu Ser Leu Asp Val Arg Lys Glu Leu Leu
 340 345 350
 40 Thr Lys Asp Leu Arg Gly Glu Met Thr Pro Pro Ser Val
 355 360 365

(10) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:365 amino acids

(B) TYPE:amino acid

(D) TOPOLOGY:linear

(ii) MOLECULAR TYPE:peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:9:

55 Met Ala Arg Ala Val Gly Pro Glu Arg Arg Leu Leu Ala Val Tyr Thr
 1 5 10 15
 Gly Gly Thr Ile Gly Met Arg Ser Glu Leu Gly Val Leu Val Pro Gly
 20 25 30
 Thr Gly Leu Ala Ala Ile Leu Arg Thr Leu Pro Met Phe His Asp Glu

5 35 40 45
 Glu His Ala Arg Ala Arg Gly Leu Ser Glu Asp Thr Leu Val Leu Pro
 50 55 60
 Pro Asp Ser Arg Asn Gln Arg Ile Leu Tyr Thr Val Leu Glu Cys Gln
 65 70 75 80
 Pro Leu Phe Asp Ser Ser Asp Met Thr Ile Ala Glu Trp Val Arg Val
 85 90 95
 10 Ala Gln Thr Ile Lys Arg His Tyr Glu Gln Tyr His Gly Phe Val Val
 100 105 110
 Ile His Gly Thr Asp Thr Met Ala Phe Ala Ala Ser Met Leu Ser Phe
 115 120 125
 Met Leu Glu Asn Leu Gln Lys Thr Val Ile Leu Thr Gly Ala Gln Val
 130 135 140
 15 Pro Ile His Ala Leu Trp Ser Asp Gly Arg Glu Asn Leu Leu Gly Ala
 145 150 155 160
 Leu Leu Met Ala Gly Gln Tyr Val Ile Pro Glu Val Cys Leu Phe Phe
 165 170 175
 Gln Asn Gln Leu Phe Arg Gly Asn Arg Ala Thr Lys Val Asp Ala Arg
 180 185 190
 20 Arg Phe Ala Ala Phe Cys Ser Pro Asn Leu Leu Pro Leu Ala Thr Val
 195 200 205
 Gly Ala Asp Ile Thr Ile Asn Arg Glu Leu Val Arg Lys Val Asp Gly
 210 215 220
 Lys Ala Gly Leu Val Val His Ser Ser Met Glu Gln Asp Val Gly Leu
 225 230 235 240
 25 Leu Arg Leu Tyr Pro Gly Ile Pro Ala Ala Leu Val Arg Ala Phe Leu
 245 250 255
 Gln Pro Pro Leu Lys Gly Val Val Met Glu Thr Phe Gly Ser Gly Asn
 260 265 270
 Gly Pro Thr Lys Pro Asp Leu Leu Gln Glu Leu Arg Val Ala Thr Glu
 275 280 285
 30 Arg Gly Leu Val Ile Val Asn Cys Thr Gln Cys Leu Gln Gly Ala Val
 290 295 300
 Thr Thr Asp Tyr Ala Ala Gly Met Ala Met Ala Gly Ala Gly Val Ile
 305 310 315 320
 Ser Gly Phe Asp Met Thr Ser Glu Ala Ala Leu Ala Lys Leu Ser Tyr
 325 330 335
 35 Val Leu Gly Gln Pro Gly Leu Ser Leu Asp Val Arg Lys Glu Leu Leu
 340 345 350
 Thr Lys Asp Leu Arg Gly Glu Met Thr Pro Pro Ser Val
 355 360 365

(11) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1089 base pairs

(B) TYPE:nucleic acid

(D) TOPOLOGY:linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:10:

ATGGCGCGCG CATCAGGCTC CGAGAGGCAC CTGCTGCTCA TCTACACTGG CGGCACTTTG 60
 GGCATGCAGA GCAAGGGCGG GGTGCTCGTC CCCGGCCCAG GCCTGGTCAC TCTGCTGCGG 120
 50 ACCCTGCCCA TGTTCCATGA CAAGGAGTTC GCCCAGGCCC AGGGCCTCCC TGACCATGCT 180
 CTGGCGCTGC CCCCTGCCAG CCACGGCCCC AGGGTCCTCT ACACGGTGCT GGAGTGCCAG 240
 CCCCTCTTGG ATTCCAGCGA CATGACCATC GATGATTGGA TTCGCATAGC CAAGATCATA 300

5 GAGAGGCACT ATGAGCAGTA CCAAGGCTTT GTGGTTATCC ACGGCACCGA CACCATGGCC 360
 TTTGGGGCCT CCATGCTGTC CTTCATGCTG GAAAACCTGC ACAAACCAGT CATCCTCACT 420
 GGC GCCCAGG TGCCAATCCG TGTGCTGTGG AATGACGCCC GGGAAAACCT GCTGGGGGCG 480
 TTGCTTGTGG CCGGCCAATA CATCATCCCT GAGGTCTGCC TGTTTATGAA CAGTCAGCTG 540
 TTTCGGGGAA ACCGGGTAAC CAAGGTGGAC TCCCAGAAGT TTGAGGCCTT CTGCTCCCCC 600
 AATCTGTCCC CACTAGCCAC TGTGGGCGCG GATGTCACAA TTGCCTGGGA CCTGGTGCGC 660
 AAGGTCAACT GGAAGGACCC GCTGGTGGTG CACAGCAACA TGGAGCACGA CGTGGCACTG 720
 CTGCGCCTCT ACCCTGGCAT CCCGGCCTCC CTGGTCCGGG CATTCTGCA GCCCCGCTC 780
 10 AAGGGCGTGG TCCTGGAGAC CTTCGGCTCT GGCAACGGGC CGAGCAAGCC CGACCTGCTG 840
 CAGGAGTTGC GGGCCGCGGC CCAGCGCGGC CTCATCATGG TCAACTGCAG CCAGTGCCTG 900
 CGGGGGTCTG TGACCCCGGG CTATGCCACG AGCTTGGCGG GCGCCAACAT CGTGTCGGC 960
 TTAGACATGA CCTCAGAGGC CGCGCTGGCT AAGCTGTCCT ACGTGTGGG CCTGCCGGAG 1020
 CTGAGCCTGG AGCGCAGGCA GGAGCTGCTG GCCAAGGATC TTCGCGGGGA AATGACACTG 1080
 15 CCCACGGCA 1089

(12) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1095 base pairs

(B) TYPE:nucleic acid

(D) TOPOLOGY:linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:11:

25 ATGGCGCGCG CGGTGGGGCC CGAGCGGAGG CTGCTGGCCG TCTACACCGG CGGCACCATT 60
 GGCATGCGGA GTGAGCTCGG CGTGCTTGTG CCCGGGACGG GCCTGGCTGC CATCCTGAGG 120
 AACTGCCCCA TGTTCCATGA CGAGGAGCAC GCCCGAGCCC GCGGCCTCTC TGAGGACACC 180
 CTGGTGCTAC CCCCGGACAG CCGCAACCAG AGGATCCTCT ACACCGTGCT GGAGTGCCAG 240
 CCCCTCTTCG ACTCCAGTGA CATGACCATC GCTGAGTGGG TTCGCGTTGC CCAGACCATC 300
 AAGAGGCACT ACGAGCAGTA CCACGGCTTT GTGGTCATCC ACGGCACCGA CACCATGGCC 360
 TTTGCTGCCT CGATGCTGTC CTTCATGCTG GAGAACCTGC AGAAGACTGT CATCCTCACT 420
 30 GGGGCCCAGG TGCCCATCCA TGCCCTGTGG AGCGACGGCC GTGAGAACCT GCTGGGGGCA 480
 CTGCTCATGG CTGGCCAGTA TGTGATCCCA GAGGTCTGCC TTTTCTTCCA GAATCAGCTG 540
 TTTCGGGGCA ACCGGGCAAC CAAGGTAGAC GCTCGGAGGT TCGCAGCTTT CTGCTCCCCG 600
 AACCTGTGTC CTCTGGCCAC AGTGGGTGCT GACATCACAA TCAACAGGGA GCTGGTGCGG 660
 AAGGTGGACG GGAAGGCTGG GCTGGTGGTG CACAGCAGCA TGGAGCAGGA CGTGGGCCTG 720
 CTGCGCCTCT ACCCTGGGAT CCCTGCCGCC CTGGTTCGGG CCTTCTTGCA GCCTCCCCTG 780
 35 AAGGGCGTGG TCATGGAGAC CTTCGGTTCA GGGAACGGAC CCACCAAGCC CGACCTGCTG 840
 CAGGAGCTGC GGGTGGCCAC CGAGCGCGGC CTGGTCATCG TCAACTGTAC CCAGTGCCTC 900
 CGGGGGGCTG TGACCACAGA CTATGCAGCT GGCATGGCCA TGGCGGGAGC CAACGTCATC 960
 TCAGGCTTCG ACATGACATC GGAGGCCGCC CTGGCCAAGC TATCGTATGT GCTGGGCCAG 1020
 CCAGGGCTGA GCCTGGATGT CAGGAAGGAG CTGCTGACCA AGGACCTTCG GGGGGAGATG 1080
 40 ACGCCACCCT CGGTG 1095

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1095 base pairs

(B) TYPE:nucleic acid

(D) TOPOLOGY:linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:12:

50 ATGGCGCGCG CGGTGGGGCC CGAGCGGAGG CTGCTGGCCG TCTACACCGG CGGCACCATT 60
 GGCATGCGGA GTGAGCTCGG CGTGCTTGTG CCCGGGACGG GCCTGGCTGC CATCCTGAGG 120
 AACTGCCCCA TGTTCCATGA CGAGGAGCAC GCCCGAGCCC GCGGCCTCTC TGAGGACACC 180

CTGGTGCTAC CCCC GGACAG CCGCAACCAG AGGATCCTCT ACACCGTGCT GGAGTGCCAG 240
 CCCCTCTTCG ACTCCAGTGA CATGACCATC GCTGAGTGGG TTCGCGTTGC CCAGACCATC 300
 AAGAGGCACT ACGAGCAGTA CCACGGCTTT GTGGTCATCC ACGGCACCGA CACCATGGCC 360
 TTTGCTGCCT CGATGCTGTC CTTTCATGCTG GAGAACCTGC AGAAGACTGT CATCCTCACT 420
 GGGGCCCAGG TGCCCATCCA TGCCCTGTGG AGCGACGGCC GTGAGAACCT GCTGGGGGCA 480
 CTGCTCATGG CTGGCCAGTA TGTGATCCCA GAGGTCTGCC TTTTCTTCCA GAATCAGCTG 540
 TTTCGGGGCA ACCGGGCAAC CAAGGTAGAC GCTCGGAGGT TCGCAGCTTT CTGCTCCCCG 600
 AACCTGCTGC CTCTGGCCAC AGTGGGTGCT GACATCACAA TCAACAGGGA GCTGGTGCGG 660
 AAGGTGGACG GGAAGGCTGG GCTGGTGGTG CACAGCAGCA TGGAGCAGGA CGTGGGCCTG 720
 CTGCGCCTCT ACCCTGGGAT CCCTGCCGCC CTGGTTCGGG CCTTCTTGCA GCCTCCCCCTG 780
 AAGGGCGTGG TCATGGAGAC CTTTCGGTTCA GGAACCGGAC CCACCAAGCC CGACCTGCTG 840
 CAGGAGCTGC GGGTGGCCAC CGAGCGCGGC CTGGTCATCG TCAACTGTAC CCAGTGCCTC 900
 CGGGGGGCTG TGACCACAGA CTATGCAGCT GGCATGGCCA TGGCGGGAGC CGGCGTCATC 960
 TCAGGCTTCG ACATGACATC GGAGGCCGCC CTGGCCAAGC TATCGTATGT GCTGGGGCCAG 1020
 CCAGGGCTGA GCCTGGATGT CAGGAAGGAG CTGCTGACCA AGGACCTTCG GGGGGAGATG 1080
 ACGCCACCCT CGGTG 1095

(14) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1095 base pairs

(B) TYPE:nucleic acid

(D) TOPOLOGY:linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:13:

ATGGCGCGCG CGGTGGGGCC CGAGCGGAGG CTGCTGGCCG TCTACACCGG CGGCACCATT 60
 GGCATGCGGA GTGAGCTCGG CGTGCTTGTTG CCCGGGACGG GCCTGGCTGC CATCCTGAGG 120
 ACACTGCCCA TGTTCCATGA CGAGGAGCAC GCCCGAGCCC GCGGCCTCTC TGAGGACACC 180
 CTGGTGCTAC CCCC GGACAG CCGCAACCAG AGGATCCTCT ACACCGTGCT GGAGTGCCAG 240
 CCCCTCTTCG ACTCCAGTGA CATGACCATC GCTGAGTGGG TTCGCGTTGC CCAGACCATC 300
 AAGAGGCACT ACGAGCAGTA CCACGGCTTT GTGGTCATCC ACGGCACCGA CACCATGGCC 360
 TTTGCTGCCT CGATGCTGTC CTTTCATGCTG GAGAACCTGC AGAAGACTGT CATCCTCACT 420
 GGGGCCCAGG TGCCCATCCA TGCCCTGTGG AGCGACGGCC GTGAGAACCT GCTGGGGGCA 480
 CTGCTCATGG CTGGCCAGTA TGTGATCCCA GAGGTCTGCC TTTTCTTCCA GAATCAGCTG 540
 TTTTCGGGGCA ACCGGGCAAC CAAGGTAGAC GCTCGGAGGT TCGCAGCTTT CTGCTCCCCG 600
 AACCTGCTGC CTCTGGCCAC AGTGGGTGCT GACATCACAA TCAACAGGGA GCTGGTGCGG 660
 AAGGTGGACG GGAAGGCTGG GCTGGTGGTG CACAGCAGCA TGGAGCAGGA CGTGGGCCTG 720
 CTGCGCCTCT ACCCTGGGAT CCCTGCCGCC CTGGTTCGGG CCTTCTTGCA GCCTCCCCCTG 780
 AAGGGCGTGG TCATGGAGAC CTTTCGGTTCA GGAACCGGAC CCACCAAGCC CGACCTGCTG 840
 CAGGAGCTGC GGGTGGCCAC CGAGCGCGGC CTGGTCATCG TCAACTGTAC CCAGTGCCTC 900
 CAGGGGGCTG TGACCACAGA CTATGCAGCT GGCATGGCCA TGGCGGGAGC CAACGTCATC 960
 TCAGGCTTCG ACATGACATC GGAGGCCGCC CTGGCCAAGC TATCGTATGT GCTGGGGCCAG 1020
 CCAGGGCTGA GCCTGGATGT CAGGAAGGAG CTGCTGACCA AGGACCTTCG GGGGGAGATG 1080
 ACGCCACCCT CGGTG 1095

(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1095 base pairs

(B) TYPE:nucleic acid

(D) TOPOLOGY:linear

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:14:

ATGGCGCGCG CGGTGGGGCC CGAGCGGAGG CTGCTGGCCG TCTACACCGG CGGCACCATT 60
 GGCATGCGGA GTGAGCTCGG CGTGCTTGTTG CCCGGGACGG GCCTGGCTGC CATCCTGAGG 120

5
 10
 15
 180
 240
 300
 360
 420
 480
 540
 600
 660
 720
 780
 840
 900
 960
 1020
 1080
 1095

(16) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:1928 base pairs
 (B) TYPE:nucleic acid
 (C) STRANDEDNESS:double
 (D) TOPOLOGY:linear

(ii) MOLECULE TYPE:cDNA to mRNA

(iii) HYPOTHETICAL:No

(iv) ANTI-SENSE:No

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:guinea pig
 (F) TISSUE TYPE:liver

(ix) FEATURE:

- (A) NAME/KEY:5'UTR
 (B) LOCATION:1..19
 (C) IDENTIFICATION METHODS:S
 (A) NAME/KEY:mat peptide
 (B) LOCATION:20..1714
 (C) IDENTIFICATION METHODS:S
 (A) NAME/KEY:3'UTR
 (B) LOCATION:1715..1928
 (C) IDENTIFICATION METHODS:S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

40
 45
 50
 55

GAGTGGCTTA GCCGCAGGC ATG GCG CGC GCA TCA GGC TCC GAG AGG CAC 49
 Met Ala Arg Ala Ser Gly Ser Glu Arg His
 1 5 10
 CTG CTG CTC ATC TAC ACT GGC GGC ACT TTG GGC ATG CAG AGC AAG GGC 97
 Leu Leu Leu Ile Tyr Thr Gly Gly Thr Leu Gly Met Gln Ser Lys Gly
 15 20 25
 GGG GTG CTC GTC CCC GGC CCA GGC CTG GTC ACT CTG CTG CGG ACC CTG 145
 Gly Val Leu Val Pro Gly Pro Gly Leu Val Thr Leu Leu Arg Thr Leu
 30 35 40
 CCC ATG TTC CAT GAC AAG GAG TTC GCC CAG GCC CAG GGC CTC CCT GAC 193
 Pro Met Phe His Asp Lys Glu Phe Ala Gln Ala Gln Gly Leu Pro Asp
 45 50 55
 CAT GCT CTG GCG CTG CCC CCT GCC AGC CAC GGC CCC AGG GTC CTC TAC 241

	His	Ala	Leu	Ala	Leu	Pro	Pro	Ala	Ser	His	Gly	Pro	Arg	Val	Leu	Tyr	
	60						65					70					
5	ACG	GTG	CTG	GAG	TGC	CAG	CCC	CTC	TTG	GAT	TCC	AGC	GAC	ATG	ACC	ATC	289
	Thr	Val	Leu	Glu	Cys	Gln	Pro	Leu	Leu	Asp	Ser	Ser	Asp	Met	Thr	Ile	
	75					80					85					90	
	GAT	GAT	TGG	ATT	CGC	ATA	GCC	AAG	ATC	ATA	GAG	AGG	CAC	TAT	GAG	CAG	337
	Asp	Asp	Trp	Ile	Arg	Ile	Ala	Lys	Ile	Ile	Glu	Arg	His	Tyr	Glu	Gln	
					95					100					105		
10	TAC	CAA	GGC	TTT	GTG	GTT	ATC	CAC	GGC	ACC	GAC	ACC	ATG	GCC	TTT	GGG	385
	Tyr	Gln	Gly	Phe	Val	Val	Ile	His	Gly	Thr	Asp	Thr	Met	Ala	Phe	Gly	
				110					115						120		
	GCC	TCC	ATG	CTG	TCC	TTC	ATG	CTG	GAA	AAC	CTG	CAC	AAA	CCA	GTC	ATC	433
	Ala	Ser	Met	Leu	Ser	Phe	Met	Leu	Glu	Asn	Leu	His	Lys	Pro	Val	Ile	
			125					130					135				
15	CTC	ACT	GGC	GCC	CAG	GTG	CCA	ATC	CGT	GTG	CTG	TGG	AAT	GAC	GCC	CGG	481
	Leu	Thr	Gly	Ala	Gln	Val	Pro	Ile	Arg	Val	Leu	Trp	Asn	Asp	Ala	Arg	
		140					145					150					
	GAA	AAC	CTG	CTG	GGG	GCG	TTG	CTT	GTG	GCC	GGC	CAA	TAC	ATC	ATC	CCT	529
	Glu	Asn	Leu	Leu	Gly	Ala	Leu	Leu	Val	Ala	Gly	Gln	Tyr	Ile	Ile	Pro	
20	155				160					165					170		
	GAG	GTC	TGC	CTG	TTT	ATG	AAC	AGT	CAG	CTG	TTT	CGG	GGA	AAC	CGG	GTA	577
	Glu	Val	Cys	Leu	Phe	Met	Asn	Ser	Gln	Leu	Phe	Arg	Gly	Asn	Arg	Val	
				175					180					185			
	ACC	AAG	GTG	GAC	TCC	CAG	AAG	TTT	GAG	GCC	TTC	TGC	TCC	CCC	AAT	CTG	625
	Thr	Lys	Val	Asp	Ser	Gln	Lys	Phe	Glu	Ala	Phe	Cys	Ser	Pro	Asn	Leu	
25				190					195					200			
	TCC	CCA	CTA	GCC	ACT	GTG	GGC	GCG	GAT	GTC	ACA	ATT	GCC	TGG	GAC	CTG	673
	Ser	Pro	Leu	Ala	Thr	Val	Gly	Ala	Asp	Val	Thr	Ile	Ala	Trp	Asp	Leu	
			205				210					215					
	GTG	CGC	AAG	GTC	AAC	TGG	AAG	GAC	CCG	CTG	GTG	GTG	CAC	AGC	AAC	ATG	721
	Val	Arg	Lys	Val	Asn	Trp	Lys	Asp	Pro	Leu	Val	Val	His	Ser	Asn	Met	
30	220					225						230					
	GAG	CAC	GAC	GTG	GCA	CTG	CTG	CGC	CTC	TAC	CCT	GGC	ATC	CCG	GCC	TCC	769
	Glu	His	Asp	Val	Ala	Leu	Leu	Arg	Leu	Tyr	Pro	Gly	Ile	Pro	Ala	Ser	
	235				240					245					250		
	CTG	GTC	CGG	GCA	TTC	CTG	CAG	CCC	CCG	CTC	AAG	GGC	GTG	GTC	CTG	GAG	817
35	Leu	Val	Arg	Ala	Phe	Leu	Gln	Pro	Pro	Lys	Gly	Val	Val	Val	Leu	Glu	
				255					260					265			
	ACC	TTC	GGC	TCT	GGC	AAC	GGG	CCG	AGC	AAG	CCC	GAC	CTG	CTG	CAG	GAG	865
	Thr	Phe	Gly	Ser	Gly	Asn	Gly	Pro	Ser	Lys	Pro	Asp	Leu	Leu	Gln	Glu	
			270				275							280			
	TTG	CGG	GCC	GCG	GCC	CAG	CGC	GGC	CTC	ATC	ATG	GTC	AAC	TGC	AGC	CAG	913
40	Leu	Arg	Ala	Ala	Gln	Arg	Gly	Leu	Ile	Met	Val	Val	Asn	Cys	Ser	Gln	
			285				290					295					
	TGC	CTG	CGG	GGG	TCT	GTG	ACC	CCG	GGC	TAT	GCC	ACG	AGC	TTG	GCG	GGC	961
	Cys	Leu	Arg	Gly	Ser	Val	Thr	Pro	Gly	Tyr	Ala	Thr	Ser	Leu	Ala	Gly	
		300				305						310					
	GCC	AAC	ATC	GTG	TCC	GGC	TTA	GAC	ATG	ACC	TCA	GAG	GCC	GCG	CTG	GCT	1009
45	Ala	Asn	Ile	Val	Ser	Gly	Leu	Asp	Met	Thr	Ser	Glu	Ala	Ala	Leu	Ala	
	315				320					325					330		
	AAG	CTG	TCC	TAC	GTG	TTG	GGC	CTG	CCG	GAG	CTG	AGC	CTG	GAG	CGC	AGG	1057
	Lys	Leu	Ser	Tyr	Val	Leu	Gly	Leu	Pro	Glu	Leu	Ser	Leu	Glu	Arg	Arg	
				335					340					345			
	CAG	GAG	CTG	CTG	GCC	AAG	GAT	CTT	CGC	GGG	GAA	ATG	ACA	CTG	CCC	ACG	1105
50	Gln	Glu	Leu	Leu	Ala	Lys	Asp	Leu	Arg	Gly	Glu	Met	Thr	Leu	Pro	Thr	
				350			355							360			
	GCA	GAC	CTG	CAC	CAG	TCC	TCT	CCG	CCG	GGC	AGC	ACA	CTG	GGG	CAA	GGT	1153

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	Ala	Asp	Leu	His	Gln	Ser	Ser	Pro	Pro	Gly	Ser	Thr	Leu	Gly	Gln	Gly	
			365					370					375				
5	GTC	GCC	CGG	CTC	TTT	AGT	CTG	TTC	GGT	TGC	CAG	GAG	GAA	GAT	TCG	GTG	1201
	Val	Ala	Arg	Leu	Phe	Ser	Leu	Phe	Gly	Cys	Gln	Glu	Glu	Asp	Ser	Val	
			380				385					390					
	CAG	GAC	GCC	GTG	ATG	CCC	AGC	CTG	GCC	CTG	GCC	TTG	GCC	CAT	GCT	GGT	1249
	Gln	Asp	Ala	Val	Met	Pro	Ser	Leu	Ala	Leu	Ala	Leu	Ala	His	Ala	Gly	
			395			400					405					410	
10	GAA	CTC	GAG	GCT	CTG	CAG	GCA	CTT	ATG	GAG	CTG	GGC	AGT	GAC	CTG	CGC	1297
	Glu	Leu	Glu	Ala	Leu	Gln	Ala	Leu	Met	Glu	Leu	Gly	Ser	Asp	Leu	Arg	
					415					420						425	
	CTA	AAG	GAC	TCT	AAT	GGC	CAA	ACC	CTG	TTG	CAT	GTG	GCT	GCT	CGG	AAT	1345
	Leu	Lys	Asp	Ser	Asn	Gly	Gln	Thr	Leu	Leu	His	Val	Ala	Ala	Arg	Asn	
				430					435						440		
15	GGG	CGT	GAT	GGC	GTG	GTC	ACC	ATG	CTG	CTG	CAC	AGA	GGC	ATG	GAT	GTC	1393
	Gly	Arg	Asp	Gly	Val	Val	Thr	Met	Leu	Leu	His	Arg	Gly	Met	Asp	Val	
			445					450				455					
	AAT	GCC	CGA	GAC	CGA	GAC	GGC	CTC	AGC	CCA	CTG	CTG	TTG	GCT	GTA	CAG	1441
	Asn	Ala	Arg	Asp	Arg	Asp	Gly	Leu	Ser	Pro	Leu	Leu	Leu	Ala	Val	Gln	
			460				465					470					
20	GGC	AGG	CAT	CGG	GAA	TGC	ATC	AGG	CTG	CTG	CGG	AAG	GCT	GGG	GCC	TGC	1489
	Gly	Arg	His	Arg	Glu	Cys	Ile	Arg	Leu	Leu	Arg	Lys	Ala	Gly	Ala	Cys	
						480					485					490	
	CTG	TCC	CCC	CAG	GAC	CTG	AAG	GAT	GCA	GGG	ACC	GAG	CTG	TGC	AGG	CTG	1537
	Leu	Ser	Pro	Gln	Asp	Leu	Lys	Asp	Ala	Gly	Thr	Glu	Leu	Cys	Arg	Leu	
					495					500						505	
25	GCA	TCC	AGG	GCT	GAC	ATG	GAA	GGC	CTG	CAG	GCA	TGG	GGG	CAG	GCT	GGG	1585
	Ala	Ser	Arg	Ala	Asp	Met	Glu	Gly	Leu	Gln	Ala	Trp	Gly	Gln	Ala	Gly	
				510					515					520			
	GCC	GAC	CTG	CAG	CAG	CCG	GGC	TAT	GAT	GGG	CGC	AGC	GCT	CTG	TGT	GTC	1633
	Ala	Asp	Leu	Gln	Gln	Pro	Gly	Tyr	Asp	Gly	Arg	Ser	Ala	Leu	Cys	Val	
				525				530				535					
30	GCA	GAA	GCA	GCC	GGG	AAC	CAG	GAG	GTG	CTG	GCC	CTT	CTG	CGG	AAC	CTG	1681
	Ala	Glu	Ala	Ala	Gly	Asn	Gln	Glu	Val	Leu	Ala	Leu	Leu	Arg	Asn	Leu	
			540				545					550					
	GCA	CTT	GTA	GGC	CCG	GAA	GTG	CCG	CCT	GCC	ATC	TGATCGCCAG	CAATCCCCGCT				1734
	Ala	Leu	Val	Gly	Pro	Glu	Val	Pro	Pro	Ala	Ile						
					555		560				565						
35	GTGGTGTGAG	CCACTCCGCC	ATCTGCTGCT	TTGACCCACT	CGAGGGACCC	TAGCACACGA											1794
	CCCCCAGCA	GGATGCACCC	CACTACTTAG	AGTATACCCC	AGGCTGGCTC	AGTGACAAGC											1854
	TGCAAAGGTC	TTTGTGGCA	GAACAGCAAT	AAAGTAACTA	CAGAGTGGCC	AAAAAAAAAA											1914
	AAAAAAAAAA	AAAA															1928

(17) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2096 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: human

(F) TISSUE TYPE: liver

(ix) FEATURE:

(A) NAME/KEY: 5' UTR

(B) LOCATION: 1..92

(C) IDENTIFICATION METHODS: S

(A) NAME/KEY: mat peptide

(B) LOCATION: 93..1811

(C) IDENTIFICATION METHODS: S

(A) NAME/KEY: 3' UTR

(B) LOCATION: 1812..2096

(C) IDENTIFICATION METHODS: S

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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CGCCCCGGGC CTCCTCCGCG CAGTCCCTGA GTCCCGCAGG CCCTGCGTCC CCGCTGCACA 60
CCCCCGTCCA CTCCCGTGGT CCCCAGTCCG GC ATG GCG CGC GCG GTG GGG CCC 113
                               1      5
                               Met Ala Arg Ala Val Gly Pro
GAG CGG AGG CTG CTG GCC GTC TAC ACC GGC GGC ACC ATT GGC ATG CGG 161
Glu Arg Arg Leu Leu Ala Val Tyr Thr Gly Gly Thr Ile Gly Met Arg
                               10      15      20
AGT GAG CTC GGC GTG CTT GTG CCC GGG ACG GGC CTG GCT GCC ATC CTG 209
Ser Glu Leu Gly Val Leu Val Pro Gly Thr Gly Leu Ala Ala Ile Leu
                               25      30      35
AGG ACA CTG CCC ATG TTC CAT GAC GAG GAG CAC GCC CGA GCC CGC GGC 257
Arg Thr Leu Pro Met Phe His Asp Glu Glu His Ala Arg Ala Arg Gly
                               40      45      50
CTC TCT GAG GAC ACC CTG GTG CTA CCC CCG GAC AGC CGC AAC CAG AGG 305
Leu Ser Glu Asp Thr Leu Val Leu Pro Pro Asp Ser Arg Asn Gln Arg
                               55      60      65
ATC CTC TAC ACC GTG CTG GAG TGC CAG CCC CTC TTC GAC TCC AGT GAC 353
Ile Leu Tyr Thr Val Leu Glu Cys Gln Pro Leu Phe Asp Ser Ser Asp
                               70      75      80
ATG ACC ATC GCT GAG TGG GTT CGC GTT GCC CAG ACC ATC AAG AGG CAC 401
Met Thr Ile Ala Glu Trp Val Arg Val Ala Gln Thr Ile Lys Arg His
                               85      90      95
TAC GAG CAG TAC CAC GGC TTT GTG GTC ATC CAC GGC ACC GAC ACC ATG 449
Tyr Glu Gln Tyr His Gly Phe Val Val Ile His Gly Thr Asp Thr Met
                               100      105      110
GCC TTT GCT GCC TCG ATG CTG TCC TTC ATG CTG GAG AAC CTG CAG AAG 497
Ala Phe Ala Ala Ser Met Leu Ser Phe Met Leu Glu Asn Leu Gln Lys
                               115      120      125
ACT GTC ATC CTC ACT GGG GCC CAG GTG CCC ATC CAT GCC CTG TGG AGC 545
Thr Val Ile Leu Thr Gly Ala Gln Val Pro Ile His Ala Leu Trp Ser
                               130      135      140
GAC GGC CGT GAG AAC CTG CTG GGG GCA CTG CTC ATG GCT GGC CAG TAT 593
Asp Gly Arg Glu Asn Leu Leu Gly Ala Leu Leu Met Ala Gly Gln Tyr
                               145      150      155
GTG ATC CCA GAG GTC TGC CTT TTC TTC CAG AAT CAG CTG TTT CGG GGC 641
Val Ile Pro Glu Val Cys Leu Phe Phe Gln Asn Gln Leu Phe Arg Gly
                               160      165      170
AAC CGG GCA ACC AAG GTA GAC GCT CGG AGG TTC GCA GCT TTC TGC TCC 689
Asn Arg Ala Thr Lys Val Asp Ala Arg Arg Phe Ala Ala Phe Cys Ser
                               175      180      185
CCG AAC CTG CTG CCT CTG GCC ACA GTG GGT GCT GAC ATC ACA ATC AAC 737
Pro Asn Leu Leu Pro Leu Ala Thr Val Gly Ala Asp Ile Thr Ile Asn
                               190      195      200
AGG GAG CTG GTG CGG AAG GTG GAC GGG AAG GCT GGG CTG GTG GTG CAC 785
                               205      210      215

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	Arg	Glu	Leu	Val	Arg	Lys	Val	Asp	Gly	Lys	Ala	Gly	Leu	Val	Val	His	
					220					225					230		
5	AGC	AGC	ATG	GAG	CAG	GAC	GTG	GGC	CTG	CTG	CGC	CTC	TAC	CCT	GGG	ATC	833
	Ser	Ser	Met	Glu	Gln	Asp	Val	Gly	Leu	Leu	Arg	Leu	Tyr	Pro	Gly	Ile	
				235					240					245			
	CCT	GCC	GCC	CTG	GTT	CGG	GCC	TTC	TTG	CAG	CCT	CCC	CTG	AAG	GGC	GTG	881
	Pro	Ala	Ala	Leu	Val	Arg	Ala	Phe	Leu	Gln	Pro	Pro	Leu	Lys	Gly	Val	
				250					255				260				
10	GTC	ATG	GAG	ACC	TTC	GGT	TCA	GGG	AAC	GGA	CCC	ACC	AAG	CCC	GAC	CTG	929
	Val	Met	Glu	Thr	Phe	Gly	Ser	Gly	Asn	Gly	Pro	Thr	Lys	Pro	Asp	Leu	
		265					270					275					
	CTG	CAG	GAG	CTG	CGG	GTG	GCC	ACC	GAG	CGC	GGC	CTG	GTC	ATC	GTC	AAC	977
	Leu	Gln	Glu	Leu	Arg	Val	Ala	Thr	Glu	Arg	Gly	Leu	Val	Ile	Val	Asn	
	280					285					290					295	
15	TGT	ACC	CAC	TGC	CTC	CAG	GGG	GCT	GTG	ACC	ACA	GAC	TAT	GCA	GCT	GGC	1025
	Cys	Thr	His	Cys	Gln	Gly	Ala	Val	Thr	Thr	Asp	Tyr	Ala	Ala	Gly		
				300						305					310		
	ATG	GCC	ATG	GCG	GGA	GCC	GGC	GTC	ATC	TCA	GGC	TTC	GAC	ATG	ACA	TCG	1073
	Met	Ala	Met	Ala	Gly	Ala	Gly	Val	Ile	Ser	Gly	Phe	Asp	Met	Thr	Ser	
				315					320					325			
20	GAG	GCC	GCC	CTG	GCC	AAG	CTA	TCG	TAT	GTG	CTG	GGC	CAG	CCA	GGG	CTG	1121
	Glu	Ala	Ala	Leu	Ala	Lys	Leu	Ser	Tyr	Val	Leu	Gly	Gln	Pro	Gly	Leu	
				330					335				340				
	AGC	CTG	GAT	GTC	AGG	AAG	GAG	CTG	CTG	ACC	AAG	GAC	CTT	CGG	GGG	GAG	1169
	Ser	Leu	Asp	Val	Arg	Lys	Glu	Leu	Leu	Thr	Lys	Asp	Leu	Arg	Gly	Glu	
		345					350					355					
25	ATG	ACG	CCA	CCC	TCG	GTG	GAA	GAG	CGC	CGG	CCC	TCA	CTG	CAG	GGC	AAC	1217
	Met	Thr	Pro	Pro	Ser	Val	Glu	Glu	Arg	Arg	Pro	Ser	Leu	Gln	Gly	Asn	
						365					370				375		
	ACG	CTG	GGC	GGT	GGG	GTC	TCC	TGG	CTC	CTC	AGT	CTG	AGC	GGC	AGC	CAG	1265
	Thr	Leu	Gly	Gly	Gly	Val	Ser	Trp	Leu	Leu	Ser	Leu	Ser	Gly	Ser	Gln	
					380					385					390		
30	GAG	GCA	GAT	GCC	CTG	CGG	AAT	GCC	CTG	GTG	CCC	AGC	CTG	GCC	TGT	GCT	1313
	Glu	Ala	Asp	Ala	Leu	Arg	Asn	Ala	Leu	Val	Pro	Ser	Leu	Ala	Cys	Ala	
				395					400					405			
	GCT	GCC	CAC	GCC	GGT	GAC	GTG	GAG	GCG	CTG	CAG	GCG	CTT	GTG	GAG	CTG	1361
	Ala	Ala	His	Ala	Gly	Asp	Val	Glu	Ala	Leu	Gln	Ala	Leu	Val	Glu	Leu	
				410					415				420				
35	GGC	AGT	GAC	CTG	GGC	CTG	GTG	GAC	TTT	AAC	GGC	CAA	ACC	CCA	CTG	CAC	1409
	Gly	Ser	Asp	Leu	Gly	Leu	Val	Asp	Phe	Asn	Gly	Gln	Thr	Pro	Leu	His	
		425					430					435					
	GCG	GCC	GCC	CGG	GGA	GGC	CAC	ACA	GAG	GCA	GTC	ACC	ATG	CTG	CTG	CAG	1457
	Ala	Ala	Ala	Arg	Gly	Gly	His	Thr	Glu	Ala	Val	Thr	Met	Leu	Leu	Gln	
					445						450				455		
40	AGA	GGT	GTG	GAC	GTG	AAC	ACC	CGG	GAC	ACG	GAT	GGC	TTC	AGC	CCG	CTG	1505
	Arg	Gly	Val	Asp	Val	Asn	Thr	Arg	Asp	Thr	Asp	Gly	Phe	Ser	Pro	Leu	
					460					465					470		
	CTG	CTG	GCC	GTG	CGG	GGC	AGG	CAT	CCG	GGT	GTC	ATT	GGG	TTG	CTG	CGG	1553
	Leu	Leu	Ala	Val	Arg	Gly	Arg	His	Pro	Gly	Val	Ile	Gly	Leu	Leu	Arg	
				475					480					485			
45	GAA	GCC	GGG	GCC	TCC	CTG	TCC	ACC	CAG	GAG	CTG	GAG	GAA	GCA	GGG	ACG	1601
	Glu	Ala	Gly	Ala	Ser	Leu	Ser	Thr	Gln	Glu	Leu	Glu	Glu	Ala	Gly	Thr	
				490					495				500				
	GAG	CTG	TGC	AGG	CTG	GCA	TAC	AGG	GCC	GAC	CTC	GAA	GGC	CTG	CAG	GTG	1649
	Glu	Leu	Cys	Arg	Leu	Ala	Tyr	Arg	Ala	Asp	Leu	Glu	Gly	Leu	Gln	Val	
		505					510					515					
50	TGG	TGG	CAG	GCA	GGG	GCT	GAC	CTG	GGG	CAG	CCG	GGC	TAT	GAC	GGG	CAC	1697

5 Trp Trp Gln Ala Gly Ala Asp Leu Gly Gln Pro Gly Tyr Asp Gly His
 520 525 530 535
 AGC GCC CTG CAC GTC GCA GAG GCA GCC GGG AAC CTG GCA GTG GTG GCC 1745
 Ser Ala Leu His Val Ala Glu Ala Ala Gly Asn Leu Ala Val Val Ala
 540 545 550
 TTT CTA CAG AGC CTG GAG GGT GCG GTT GGT GCC CAG GCC CCA TGC CCA 1793
 Phe Leu Gln Ser Leu Glu Gly Ala Val Gly Ala Gln Ala Pro Cys Pro
 555 560 565
 10 GAA GTG CTG CCT GGT GTC TAACCTGAAG GCGTCTTGCT GCAGTATAAG 1841
 Glu Val Leu Pro Gly Val
 570
 CCATTCCTTC CTCCCATGAC CTGCTGGAGG GGTCTCAGGC ATGACCCAC TGCTGGGGCT 1901
 GCTTCCCAGC CTGCTCTCAT GTAAAGCCTG AAGGCCTTTG TTGGGCAGGA CGGCAATAAA 1961
 15 GTCTCTGACA TCCCCTCACC AGGTCTGTAC AGCCTGGCTC TGAGAGGCTC TGTCTGGGTC 2021
 CGGGACTGTG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2081
 AAAAAAAAAA AAAAA 2096

(18) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1695 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: guinea pig
 (F) TISSUE TYPE: liver

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
 (B) LOCATION: 1..1695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

35 ATG GCG CGC GCA TCA GGC TCC GAG AGG CAC CTG CTG CTC ATC TAC ACT 48
 Met Ala Arg Ala Ser Gly Ser Glu Arg His Leu Leu Leu Ile Tyr Thr
 1 5 10 15
 GGC GGC ACT TTG GGC ATG CAG AGC AAG GGC GGG GTG CTC GTC CCC GGC 96
 Gly Gly Thr Leu Gly Met Gln Ser Lys Gly Gly Val Leu Val Pro Gly
 20 25 30
 CCA GGC CTG GTC ACT CTG CTG CGG ACC CTG CCC ATG TTC CAT GAC AAG 144
 Pro Gly Leu Val Thr Leu Leu Arg Thr Leu Pro Met Phe His Asp Lys
 35 40 45
 GAG TTC GCC CAG GCC CAG GGC CTC CCT GAC CAT GCT CTG GCG CTG CCC 192
 Glu Phe Ala Gln Ala Gln Gly Leu Pro Asp His Ala Leu Ala Leu Pro
 50 55 60
 CCT GCC AGC CAC GGC CCC AGG GTC CTC TAC ACG GTG CTG GAG TGC CAG 240
 Pro Ala Ser His Gly Pro Arg Val Leu Tyr Thr Val Leu Glu Cys Gln
 65 70 75 80
 CCC CTC TTG GAT TCC AGC GAC ATG ACC ATC GAT GAT TGG ATT CGC ATA 288
 Pro Leu Leu Asp Ser Ser Asp Met Thr Ile Asp Asp Trp Ile Arg Ile
 85 90 95
 55 GCC AAG ATC ATA GAG AGG CAC TAT GAG CAG TAC CAA GGC TTT GTG GTT 336
 Ala Lys Ile Ile Glu Arg His Tyr Glu Gln Tyr Gln Gly Phe Val Val

			100				105				110						
	ATC	CAC	GGC	ACC	GAC	ACC	ATG	GCC	TTT	GGG	GCC	TCC	ATG	CTG	TCC	TTC	384
5	Ile	His	Gly	Thr	Asp	Thr	Met	Ala	Phe	Gly	Ala	Ser	Met	Leu	Ser	Phe	
			115				120						125				
	ATG	CTG	GAA	AAC	CTG	CAC	AAA	CCA	GTC	ATC	CTC	ACT	GGC	GCC	CAG	GTG	432
	Met	Leu	Glu	Asn	Leu	His	Lys	Pro	Val	Ile	Leu	Thr	Gly	Ala	Gln	Val	
			130				135						140				
10	CCA	ATC	CGT	GTG	CTG	TGG	AAT	GAC	GCC	CGG	GAA	AAC	CTG	CTG	GGG	GCG	480
	Pro	Ile	Arg	Val	Leu	Trp	Asn	Asp	Ala	Arg	Glu	Asn	Leu	Leu	Gly	Ala	
			145				150						155			160	
	TTG	CTT	GTG	GCC	GGC	CAA	TAC	ATC	ATC	CCT	GAG	GTC	TGC	CTG	TTT	ATG	528
	Leu	Leu	Val	Ala	Gly	Gln	Tyr	Ile	Ile	Pro	Glu	Val	Cys	Leu	Phe	Met	
					165					170					175		
15	AAC	AGT	CAG	CTG	TTT	CGG	GGA	AAC	CGG	GTA	ACC	AAG	GTG	GAC	TCC	CAG	576
	Asn	Ser	Gln	Leu	Phe	Arg	Gly	Asn	Arg	Val	Thr	Lys	Val	Asp	Ser	Gln	
					180					185					190		
	AAG	TTT	GAG	GCC	TTC	TGC	TCC	CCC	AAT	CTG	TCC	CCA	CTA	GCC	ACT	GTG	624
	Lys	Phe	Glu	Ala	Phe	Cys	Ser	Pro	Asn	Leu	Ser	Pro	Leu	Ala	Thr	Val	
					195				200						205		
20	GGC	GCG	GAT	GTC	ACA	ATT	GCC	TGG	GAC	CTG	GTG	CGC	AAG	GTC	AAC	TGG	672
	Gly	Ala	Asp	Val	Thr	Ile	Ala	Trp	Asp	Leu	Val	Arg	Lys	Val	Asn	Trp	
							215						220				
	AAG	GAC	CCG	CTG	GTG	GTG	CAC	AGC	AAC	ATG	GAG	CAC	GAC	GTG	GCA	CTG	720
	Lys	Asp	Pro	Leu	Val	Val	His	Ser	Asn	Met	Glu	His	Asp	Val	Ala	Leu	
							230						235			240	
25	CTG	CGC	CTC	TAC	CCT	GGC	ATC	CCG	GCC	TCC	CTG	GTC	CGG	GCA	TTC	CTG	768
	Leu	Arg	Leu	Tyr	Pro	Gly	Ile	Pro	Ala	Ser	Leu	Val	Arg	Ala	Phe	Leu	
						245					250				255		
	CAG	CCC	CCG	CTC	AAG	GGC	GTG	GTC	CTG	GAG	ACC	TTC	GGC	TCT	GGC	AAC	816
	Gln	Pro	Pro	Leu	Lys	Gly	Val	Val	Leu	Glu	Thr	Phe	Gly	Ser	Gly	Asn	
					260					265					270		
30	GGG	CCG	AGC	AAG	CCC	GAC	CTG	CTG	CAG	GAG	TTG	CGG	GCC	GCG	GCC	CAG	864
	Gly	Pro	Ser	Lys	Pro	Asp	Leu	Leu	Gln	Glu	Leu	Arg	Ala	Ala	Ala	Gln	
							280							285			
	CGC	GGC	CTC	ATC	ATG	GTC	AAC	TGC	AGC	CAG	TGC	CTG	CGG	GGG	TCT	GTG	912
	Arg	Gly	Leu	Ile	Met	Val	Asn	Cys	Ser	Gln	Cys	Leu	Arg	Gly	Ser	Val	
							295						300				
35	ACC	CCG	GGC	TAT	GCC	ACG	AGC	TTG	GCG	GGC	GCC	AAC	ATC	GTG	TCC	GGC	960
	Thr	Pro	Gly	Tyr	Ala	Thr	Ser	Leu	Ala	Gly	Ala	Asn	Ile	Val	Ser	Gly	
							310					315				320	
	TTA	GAC	ATG	ACC	TCA	GAG	GCC	GCG	CTG	GCT	AAG	CTG	TCC	TAC	GTG	TTG	1008
	Leu	Asp	Met	Thr	Ser	Glu	Ala	Ala	Leu	Ala	Lys	Leu	Ser	Tyr	Val	Leu	
						325					330				335		
40	GGC	CTG	CCG	GAG	CTG	AGC	CTG	GAG	CGC	AGG	CAG	GAG	CTG	CTG	GCC	AAG	1056
	Gly	Leu	Pro	Glu	Leu	Ser	Leu	Glu	Arg	Arg	Gln	Glu	Leu	Leu	Ala	Lys	
							340				345				350		
	GAT	CTT	CGC	GGG	GAA	ATG	ACA	CTG	CCC	ACG	GCA	GAC	CTG	CAC	CAG	TCC	1104
	Asp	Leu	Arg	Gly	Glu	Met	Thr	Leu	Pro	Thr	Ala	Asp	Leu	His	Gln	Ser	
									360				365				
45	TCT	CCG	CCG	GGC	AGC	ACA	CTG	GGG	CAA	GGT	GTC	GCC	CGG	CTC	TTT	AGT	1152
	Ser	Pro	Pro	Gly	Ser	Thr	Leu	Gly	Gln	Gly	Val	Ala	Arg	Leu	Phe	Ser	
							375						380				
	CTG	TTC	GGT	TGC	CAG	GAG	GAA	GAT	TCG	GTG	CAG	GAC	GTG	ATG	CCC		1200
	Leu	Phe	Gly	Cys	Gln	Glu	Glu	Asp	Ser	Val	Gln	Asp	Ala	Val	Met	Pro	
							390					395				400	
50	AGC	CTG	GCC	CTG	GCC	TTG	GCC	CAT	GCT	GGT	GAA	CTC	GAG	GCT	CTG	CAG	1248
	Ser	Leu	Ala	Leu	Ala	Leu	Ala	His	Ala	Gly	Glu	Leu	Glu	Ala	Leu	Gln	

55

5 GCA CTT ATG GAG CTG GGC AGT GAC CTG CGC CTA AAG GAC TCT AAT GGC 1296
Ala Leu Met Glu Leu Gly Ser Asp Leu Arg Leu Lys Asp Ser Asn Gly
420 425 430
CAA ACC CTG TTG CAT GTG GCT GCT CGG AAT GGG CGT GAT GGC GTG GTC 1344
Gln Thr Leu Leu His Val Ala Ala Arg Asn Gly Arg Asp Gly Val Val
435 440 445
10 ACC ATG CTG CTG CAC AGA GGC ATG GAT GTC AAT GCC CGA GAC CGA GAC 1392
Thr Met Leu Leu His Arg Gly Met Asp Val Asn Ala Arg Asp Arg Asp
450 455 460
GGC CTC AGC CCA CTG CTG TTG GCT GTA CAG GGC AGG CAT CGG GAA TGC 1440
Gly Leu Ser Pro Leu Leu Leu Ala Val Gln Gly Arg His Arg Glu Cys
465 470 475 480
15 ATC AGG CTG CTG CGG AAG GCT GGG GCC TGC CTG TCC CCC CAG GAC CTG 1488
Ile Arg Leu Leu Arg Lys Ala Gly Ala Cys Leu Ser Pro Gln Asp Leu
485 490 495
AAG GAT GCA GGG ACC GAG CTG TGC AGG CTG GCA TCC AGG GCT GAC ATG 1536
Lys Asp Ala Gly Thr Glu Leu Cys Arg Leu Ala Ser Arg Ala Asp Met
500 505 510
20 GAA GGC CTG CAG GCA TGG GGG CAG GCT GGG GCC GAC CTG CAG CAG CCG 1584
Glu Gly Leu Gln Ala Trp Gly Gln Ala Gly Ala Asp Leu Gln Gln Pro
515 520 525
GGC TAT GAT GGG CGC AGC GCT CTG TGT GTC GCA GAA GCA GCC GGG AAC 1632
Gly Tyr Asp Gly Arg Ser Ala Leu Cys Val Ala Glu Ala Ala Gly Asn
530 535 540
25 CAG GAG GTG CTG GCC CTT CTG CGG AAC CTG GCA CTT GTA GGC CCG GAA 1680
Gln Glu Val Leu Ala Leu Leu Arg Asn Leu Ala Leu Val Gly Pro Glu
545 550 555 560
GTG CCG CCT GCC ATC 1695
Val Pro Pro Ala Ile
565

30

(19) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:1719 base pairs

(B) TYPE:nucleic acid

(C) STRANDEDNESS:double

(D) TOPOLOGY:linear

(ii) MOLECULE TYPE:cDNA to mRNA

(iii) HYPOTHETICAL:No

(iv) ANTI-SENSE:No

(vi) ORIGINAL SOURCE:

(A) ORGANISM:human

(F) TISSUE TYPE:liver

(ix) FEATURE:

(A) NAME/KEY:mat peptide

(B) LOCATION:1..1719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

45 ATG GCG CGC GCG GTG GGG CCC GAG CGG AGG CTG CTG GCC GTC TAC ACC 48
Met Ala Arg Ala Val Gly Pro Glu Arg Arg Leu Leu Ala Val Tyr Thr
1 5 10 15
GGC GGC ACC ATT GGC ATG CGG AGT GAG CTC GGC GTG CTT GTG CCC GGG 96
Gly Gly Thr Ile Gly Met Arg Ser Glu Leu Gly Val Leu Val Pro Gly
20 25 30

50

55

5	ACG	GGC	CTG	GCT	GCC	ATC	CTG	AGG	ACA	CTG	CCC	ATG	TTC	CAT	GAC	GAG	144
	Thr	Gly	Leu	Ala	Ala	Ile	Leu	Arg	Thr	Leu	Pro	Met	Phe	His	Asp	Glu	
			35					40					45				
	GAG	CAC	GCC	CGA	GCC	CGC	GGC	CTC	TCT	GAG	GAC	ACC	CTG	GTG	CTA	CCC	192
	Glu	His	Ala	Arg	Ala	Arg	Gly	Leu	Ser	Glu	Asp	Thr	Leu	Val	Leu	Pro	
			50				55					60					
10	CCG	GAC	AGC	CGC	AAC	CAG	AGG	ATC	CTC	TAC	ACC	GTG	CTG	GAG	TGC	CAG	240
	Pro	Asp	Ser	Arg	Asn	Gln	Arg	Ile	Leu	Tyr	Thr	Val	Leu	Glu	Cys	Gln	
			65			70					75				80		
	CCC	CTC	TTC	GAC	TCC	AGT	GAC	ATG	ACC	ATC	GCT	GAG	TGG	GTT	CGC	GTT	288
	Pro	Leu	Phe	Asp	Ser	Ser	Asp	Met	Thr	Ile	Ala	Glu	Trp	Val	Arg	Val	
					85					90					95		
15	GCC	CAG	ACC	ATC	AAG	AGG	CAC	TAC	GAG	CAG	TAC	CAC	GGC	TTT	GTG	GTC	336
	Ala	Gln	Thr	Ile	Lys	Arg	His	Tyr	Glu	Gln	Tyr	His	Gly	Phe	Val	Val	
				100					105					110			
	ATC	CAC	GGC	ACC	GAC	ACC	ATG	GCC	TTT	GCT	GCC	TCG	ATG	CTG	TCC	TTC	384
	Ile	His	Gly	Thr	Asp	Thr	Met	Ala	Phe	Ala	Ala	Ser	Met	Leu	Ser	Phe	
			115					120					125				
20	ATG	CTG	GAG	AAC	CTG	CAG	AAG	ACT	GTC	ATC	CTC	ACT	GGG	GCC	CAG	GTG	432
	Met	Leu	Glu	Asn	Leu	Gln	Lys	Thr	Val	Ile	Leu	Thr	Gly	Ala	Gln	Val	
			130				135					140					
	CCC	ATC	CAT	GCC	CTG	TGG	AGC	GAC	GGC	CGT	GAG	AAC	CTG	CTG	GGG	GCA	480
	Pro	Ile	His	Ala	Leu	Trp	Ser	Asp	Gly	Arg	Glu	Asn	Leu	Leu	Gly	Ala	
			145			150					155				160		
25	CTG	CTC	ATG	GCT	GGC	CAG	TAT	GTG	ATC	CCA	GAG	GTC	TGC	CTT	TTC	TTC	528
	Leu	Leu	Met	Ala	Gly	Gln	Tyr	Val	Ile	Pro	Glu	Val	Cys	Leu	Phe	Phe	
				165						170					175		
	CAG	AAT	CAG	CTG	TTT	CGG	GGC	AAC	CGG	GCA	ACC	AAG	GTA	GAC	GCT	CGG	576
	Gln	Asn	Gln	Leu	Phe	Arg	Gly	Asn	Arg	Ala	Thr	Lys	Val	Asp	Ala	Arg	
				180					185					190			
30	AGG	TTC	GCA	GCT	TTC	TGC	TCC	CCG	AAC	CTG	CTG	CCT	CTG	GCC	ACA	GTG	624
	Arg	Phe	Ala	Ala	Phe	Cys	Ser	Pro	Asn	Leu	Leu	Pro	Leu	Ala	Thr	Val	
			195					200					205				
	GGT	GCT	GAC	ATC	ACA	ATC	AAC	AGG	GAG	CTG	GTG	CGG	AAG	GTG	GAC	GGG	672
	Gly	Ala	Asp	Ile	Thr	Ile	Asn	Arg	Glu	Leu	Val	Arg	Lys	Val	Asp	Gly	
			210				215					220					
35	AAG	GCT	GGG	CTG	GTG	GTG	CAC	AGC	AGC	ATG	GAG	CAG	GAC	GTG	GGC	CTG	720
	Lys	Ala	Gly	Leu	Val	Val	His	Ser	Ser	Met	Glu	Gln	Asp	Val	Gly	Leu	
			225			230					235				240		
	CTG	CGC	CTC	TAC	CCT	GGG	ATC	CCT	GCC	GCC	CTG	GTT	CGG	GCC	TTC	TTG	768
	Leu	Arg	Leu	Tyr	Pro	Gly	Ile	Pro	Ala	Ala	Leu	Val	Arg	Ala	Phe	Leu	
				245					250						255		
40	CAG	CCT	CCC	CTG	AAG	GGC	GTG	GTC	ATG	GAG	ACC	TTC	GGT	TCA	GGG	AAC	816
	Gln	Pro	Pro	Leu	Lys	Gly	Val	Val	Met	Glu	Thr	Phe	Gly	Ser	Gly	Asn	
				260					265					270			
	GGA	CCC	ACC	AAG	CCC	GAC	CTG	CTG	CAG	GAG	CTG	CGG	GTG	GCC	ACC	GAG	864
	Gly	Pro	Thr	Lys	Pro	Asp	Leu	Leu	Gln	Glu	Leu	Arg	Val	Ala	Thr	Glu	
			275					280					285				
45	CGC	GGC	CTG	GTC	ATC	GTC	AAC	TGT	ACC	CAC	TGC	CTC	CAG	GGG	GCT	GTG	912
	Arg	Gly	Leu	Val	Ile	Val	Asn	Cys	Thr	His	Cys	Leu	Gln	Gly	Ala	Val	
			290				295					300					
	ACC	ACA	GAC	TAT	GCA	GCT	GGC	ATG	GCC	ATG	GCG	GGA	GCC	GGC	GTC	ATC	960
	Thr	Thr	Asp	Tyr	Ala	Ala	Gly	Met	Ala	Met	Ala	Gly	Ala	Gly	Val	Ile	
			305			310					315				320		
50	TCA	GGC	TTC	GAC	ATG	ACA	TCG	GAG	GCC	GCC	CTG	GCC	AAG	CTA	TCG	TAT	1008
	Ser	Gly	Phe	Asp	Met	Thr	Ser	Glu	Ala	Ala	Leu	Ala	Lys	Leu	Ser	Tyr	
				325						330					335		

	GTG	CTG	GGC	CAG	CCA	GGG	CTG	AGC	CTG	GAT	GTC	AGG	AAG	GAG	CTG	CTG	1056
	Val	Leu	Gly	Gln	Pro	Gly	Leu	Ser	Leu	Asp	Val	Arg	Lys	Glu	Leu	Leu	
			340						345					350			
5	ACC	AAG	GAC	CTT	CGG	GGG	GAG	ATG	ACG	CCA	CCC	TCG	GTG	GAA	GAG	CGC	1104
	Thr	Lys	Asp	Leu	Arg	Gly	Glu	Met	Thr	Pro	Pro	Ser	Val	Glu	Glu	Arg	
			355						360					365			
	CGG	CCC	TCA	CTG	CAG	GGC	AAC	ACG	CTG	GGC	GGT	GGG	GTC	TCC	TGG	CTC	1152
	Arg	Pro	Ser	Leu	Gln	Gly	Asn	Thr	Leu	Gly	Gly	Gly	Val	Ser	Trp	Leu	
			370						375				380				
10	CTC	AGT	CTG	AGC	GGC	AGC	CAG	GAG	GCA	GAT	GCC	CTG	CGG	AAT	GCC	CTG	1200
	Leu	Ser	Leu	Ser	Gly	Ser	Gln	Glu	Ala	Asp	Ala	Leu	Arg	Asn	Ala	Leu	
			385								395					400	
	GTG	CCC	AGC	CTG	GCC	TGT	GCT	GCT	GCC	CAC	GCC	GGT	GAC	GTG	GAG	GCG	1248
	Val	Pro	Ser	Leu	Ala	Cys	Ala	Ala	Ala	His	Ala	Gly	Asp	Val	Glu	Ala	
					405						410					415	
15	CTG	CAG	GCG	CTT	GTG	GAG	CTG	GGC	AGT	GAC	CTG	GGC	CTG	GTG	GAC	TTT	1296
	Leu	Gln	Ala	Leu	Val	Glu	Leu	Gly	Ser	Asp	Leu	Gly	Leu	Val	Asp	Phe	
				420						425						430	
	AAC	GGC	CAA	ACC	CCA	CTG	CAC	GCG	GCC	GCC	CGG	GGA	GGC	CAC	ACA	GAG	1344
	Asn	Gly	Gln	Thr	Pro	Leu	His	Ala	Ala	Ala	Arg	Gly	Gly	His	Thr	Glu	
			435							440						445	
20	GCA	GTC	ACC	ATG	CTG	CTG	CAG	AGA	GGT	GTG	GAC	GTG	AAC	ACC	CGG	GAC	1392
	Ala	Val	Thr	Met	Leu	Leu	Gln	Arg	Gly	Val	Asp	Val	Asn	Thr	Arg	Asp	
			450						455							460	
	ACG	GAT	GGC	TTC	AGC	CCG	CTG	CTG	CTG	GCC	GTG	CGG	GGC	AGG	CAT	CCG	1440
	Thr	Asp	Gly	Phe	Ser	Pro	Leu	Leu	Leu	Ala	Val	Arg	Gly	Arg	His	Pro	
			465									475				480	
25	GGT	GTC	ATT	GGG	TTG	CTG	CGG	GAA	GCC	GGG	GCC	TCC	CTG	TCC	ACC	CAG	1488
	Gly	Val	Ile	Gly	Leu	Leu	Arg	Glu	Ala	Gly	Ala	Ser	Leu	Ser	Thr	Gln	
				485							490					495	
	GAG	CTG	GAG	GAA	GCA	GGG	ACG	GAG	CTG	TGC	AGG	CTG	GCA	TAC	AGG	GCC	1536
	Glu	Leu	Glu	Glu	Ala	Gly	Thr	Glu	Leu	Cys	Arg	Leu	Ala	Tyr	Arg	Ala	
				500						505						510	
30	GAC	CTC	GAA	GGC	CTG	CAG	GTG	TGG	TGG	CAG	GCA	GGG	GCT	GAC	CTG	GGG	1584
	Asp	Leu	Glu	Gly	Leu	Gln	Val	Trp	Trp	Gln	Ala	Gly	Ala	Asp	Leu	Gly	
			515							520						525	
	CAG	CCG	GGC	TAT	GAC	GGG	CAC	AGC	GCC	CTG	CAC	GTC	GCA	GAG	GCA	GCC	1632
	Gln	Pro	Gly	Tyr	Asp	Gly	His	Ser	Ala	Leu	His	Val	Ala	Glu	Ala	Ala	
			530							535						540	
35	GGG	AAC	CTG	GCA	GTG	GTG	GCC	TTT	CTA	CAG	AGC	CTG	GAG	GGT	GCG	GTT	1680
	Gly	Asn	Leu	Ala	Val	Val	Ala	Phe	Leu	Gln	Ser	Leu	Glu	Gly	Ala	Val	
			545									555				560	
	GGT	GCC	CAG	GCC	CCA	TGC	CCA	GAA	GTG	CTG	CCT	GGT	GTC				1716
	Gly	Ala	Gln	Ala	Pro	Cys	Pro	Glu	Val	Leu	Pro	Gly	Val				
40					565						570					573	

45 Claims

1. A polypeptide which originate from mammal, having L-asparaginase activity.
2. The polypeptide of claim 1, which is obtainable by the expression of a gene originating from mammal.
3. The polypeptide of claim 1, which has amino acid sequences of SEQ ID NOs:1 to 3 (where the symbol "Xaa" means "glutamine" or "threonine");

55

SEQ ID NO: 1:

Thr Gly Gly Thr
1

SEQ ID NO: 2:

His Gly Thr Asp Thr
1 5

SEQ ID NO: 3:

Gln Cys Leu Xaa Gly.
1 5

4. The polypeptide of claim 1, which has an amino acid sequence selected from the group consisting of SEQ ID NOS: 4 to 9 and homologous amino acid sequences thereunto;

SEQ ID NO: 4:

Met	Ala	Arg	Ala	Ser	Gly	Ser	Glu	Arg	His	Leu	Leu	Leu	Ile	Tyr	Thr
1				5					10					15	
Gly	Gly	Thr	Leu	Gly	Met	Gln	Ser	Lys	Gly	Gly	Val	Leu	Val	Pro	Gly
			20					25					30		
Pro	Gly	Leu	Val	Thr	Leu	Leu	Arg	Thr	Leu	Pro	Met	Phe	His	Asp	Lys
		35					40					45			
Glu	Phe	Ala	Gln	Ala	Gln	Gly	Leu	Pro	Asp	His	Ala	Leu	Ala	Leu	Pro
	50					55					60				

5 Pro Ala Ser His Gly Pro Arg Val Leu Tyr Thr Val Leu Glu Cys Gln
 65 70 75 80
 Pro Leu Leu Asp Ser Ser Asp Met Thr Ile Asp Asp Trp Ile Arg Ile
 85 90 95
 Ala Lys Ile Ile Glu Arg His Tyr Glu Gln Tyr Gln Gly Phe Val Val
 100 105 110
 Ile His Gly Thr Asp Thr Met Ala Phe Gly Ala Ser Met Leu Ser Phe
 115 120 125
 10 Met Leu Glu Asn Leu His Lys Pro Val Ile Leu Thr Gly Ala Gln Val
 130 135 140
 Pro Ile Arg Val Leu Trp Asn Asp Ala Arg Glu Asn Leu Leu Gly Ala
 145 150 155 160
 15 Leu Leu Val Ala Gly Gln Tyr Ile Ile Pro Glu Val Cys Leu Phe Met
 165 170 175
 Asn Ser Gln Leu Phe Arg Gly Asn Arg Val Thr Lys Val Asp Ser Gln
 180 185 190
 Lys Phe Glu Ala Phe Cys Ser Pro Asn Leu Ser Pro Leu Ala Thr Val
 195 200 205
 20 Gly Ala Asp Val Thr Ile Ala Trp Asp Leu Val Arg Lys Val Asn Trp
 210 215 220
 Lys Asp Pro Leu Val Val His Ser Asn Met Glu His Asp Val Ala Leu
 225 230 235 240
 25 Leu Arg Leu Tyr Pro Gly Ile Pro Ala Ser Leu Val Arg Ala Phe Leu
 245 250 255
 Gln Pro Pro Leu Lys Gly Val Val Leu Glu Thr Phe Gly Ser Gly Asn
 260 265 270
 Gly Pro Ser Lys Pro Asp Leu Leu Gln Glu Leu Arg Ala Ala Ala Gln
 275 280 285
 30 Arg Gly Leu Ile Met Val Asn Cys Ser Gln Cys Leu Arg Gly Ser Val
 290 295 300
 Thr Pro Gly Tyr Ala Thr Ser Leu Ala Gly Ala Asn Ile Val Ser Gly
 305 310 315 320
 Leu Asp Met Thr Ser Glu Ala Ala Leu Ala Lys Leu Ser Tyr Val Leu
 325 330 335
 35 Gly Leu Pro Glu Leu Ser Leu Glu Arg Arg Gln Glu Leu Leu Ala Lys
 340 345 350
 Asp Leu Arg Gly Glu Met Thr Leu Pro Thr Ala
 355 360 363

SEQ ID NO: 5:

5 Met Ala Arg Ala Ser Gly Ser Glu Arg His Leu Leu Leu Ile Tyr Thr
 1 5 10 15
 Gly Gly Thr Leu Gly Met Gln Ser Lys Gly Gly Val Leu Val Pro Gly
 20 25 30
 Pro Gly Leu Val Thr Leu Leu Arg Thr Leu Pro Met Phe His Asp Lys
 35 40 45
 10 Glu Phe Ala Gln Ala Gln Gly Leu Pro Asp His Ala Leu Ala Leu Pro
 50 55 60
 Pro Ala Ser His Gly Pro Arg Val Leu Tyr Thr Val Leu Glu Cys Gln
 65 70 75 80
 15 Pro Leu Leu Asp Ser Ser Asp Met Thr Ile Asp Asp Trp Ile Arg Ile
 85 90 95
 Ala Lys Ile Ile Glu Arg His Tyr Glu Gln Tyr Gln Gly Phe Val Val
 100 105 110

Ile His Gly Thr Asp Thr Met Ala Phe Gly Ala Ser Met Leu Ser Phe
 115 120 125
 5 Met Leu Glu Asn Leu His Lys Pro Val Ile Leu Thr Gly Ala Gln Val
 130 135 140
 Pro Ile Arg Val Leu Trp Asn Asp Ala Arg Glu Asn Leu Leu Gly Ala
 145 150 155 160
 Leu Leu Val Ala Gly Gln Tyr Ile Ile Pro Glu Val Cys Leu Phe Met
 165 170 175
 10 Asn Ser Gln Leu Phe Arg Gly Asn Arg Val Thr Lys Val Asp Ser Gln
 180 185 190
 Lys Phe Glu Ala Phe Cys Ser Pro Asn Leu Ser Pro Leu Ala Thr Val
 195 200 205
 Gly Ala Asp Val Thr Ile Ala Trp Asp Leu Val Arg Lys Val Asn Trp
 210 215 220
 15 Lys Asp Pro Leu Val Val His Ser Asn Met Glu His Asp Val Ala Leu
 225 230 235 240
 Leu Arg Leu Tyr Pro Gly Ile Pro Ala Ser Leu Val Arg Ala Phe Leu
 245 250 255
 20 Gln Pro Pro Leu Lys Gly Val Val Leu Glu Thr Phe Gly Ser Gly Asn
 260 265 270
 Gly Pro Ser Lys Pro Asp Leu Leu Gln Glu Leu Arg Ala Ala Gln
 275 280 285
 Arg Gly Leu Ile Met Val Asn Cys Ser Gln Cys Leu Arg Gly Ser Val
 290 295 300
 25 Thr Pro Gly Tyr Ala Thr Ser Leu Ala Gly Ala Asn Ile Val Ser Gly
 305 310 315 320
 Leu Asp Met Thr Ser Glu Ala Ala Leu Ala Lys Leu Ser Tyr Val Leu
 325 330 335
 30 Gly Leu Pro Glu Leu Ser Leu Glu Arg Gln Glu Leu Leu Ala Lys
 340 345 350
 Asp Leu Arg Gly Glu Met Thr Leu Pro Thr Ala Asp Leu His Gln Ser
 355 360 365
 Ser Pro Pro Gly Ser Thr Leu Gly Gln Gly Val Ala Arg Leu Phe Ser
 370 375 380
 35 Leu Phe Gly Cys Gln Glu Glu Asp Ser Val Gln Asp Ala Val Met Pro
 385 390 395 400
 Ser Leu Ala Leu Ala Leu Ala His Ala Gly Glu Leu Glu Ala Leu Gln
 405 410 415
 Ala Leu Met Glu Leu Gly Ser Asp Leu Arg Leu Lys Asp Ser Asn Gly
 420 425 430
 40 Gln Thr Leu Leu His Val Ala Ala Arg Asn Gly Arg Asp Gly Val Val
 435 440 445
 Thr Met Leu Leu His Arg Gly Met Asp Val Asn Ala Arg Asp Arg Asp
 450 455 460
 45 Gly Leu Ser Pro Leu Leu Ala Val Gln Gly Arg His Arg Glu Cys
 465 470 475 480
 Ile Arg Leu Leu Arg Lys Ala Gly Ala Cys Leu Ser Pro Gln Asp Leu
 485 490 495
 Lys Asp Ala Gly Thr Glu Leu Cys Arg Leu Ala Ser Arg Ala Asp Met
 500 505 510
 50 Glu Gly Leu Gln Ala Trp Gly Gln Ala Gly Ala Asp Leu Gln Gln Pro
 515 520 525
 Gly Tyr Asp Gly Arg Ser Ala Leu Cys Val Ala Glu Ala Ala Gly Asn
 530 535 540
 Gln Glu Val Leu Ala Leu Leu Arg Asn Leu Ala Leu Val Gly Pro Glu
 545 550 555 560
 Val Pro Pro Ala Ile

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SEQ ID NO: 6:

10 Met Ala Arg Ala Val Gly Pro Glu Arg Arg Leu Leu Ala Val Tyr Thr
 1 5 10
 Gly Gly Thr Ile Gly Met Arg Ser Glu Leu Gly Val Leu Val Pro Gly
 20 25 30
 15 Thr Gly Leu Ala Ala Ile Leu Arg Thr Leu Pro Met Phe His Asp Glu
 35 40 45
 Glu His Ala Arg Ala Arg Gly Leu Ser Glu Asp Thr Leu Val Leu Pro
 50 55 60
 Pro Asp Ser Arg Asn Gln Arg Ile Leu Tyr Thr Val Leu Glu Cys Gln
 65 70 75 80
 20 Pro Leu Phe Asp Ser Ser Asp Met Thr Ile Ala Glu Trp Val Arg Val
 85 90 95
 Ala Gln Thr Ile Lys Arg His Tyr Glu Gln Tyr His Gly Phe Val Val
 100 105 110
 25 Ile His Gly Thr Asp Thr Met Ala Phe Ala Ala Ser Met Leu Ser Phe
 115 120 125
 Met Leu Glu Asn Leu Gln Lys Thr Val Ile Leu Thr Gly Ala Gln Val
 130 135 140
 Pro Ile His Ala Leu Trp Ser Asp Gly Arg Glu Asn Leu Leu Gly Ala
 145 150 155 160
 30 Leu Leu Met Ala Gly Gln Tyr Val Ile Pro Glu Val Cys Leu Phe Phe
 165 170 175
 Gln Asn Gln Leu Phe Arg Gly Asn Arg Ala Thr Lys Val Asp Ala Arg
 180 185 190
 Arg Phe Ala Ala Phe Cys Ser Pro Asn Leu Leu Pro Leu Ala Thr Val
 195 200 205
 35 Gly Ala Asp Ile Thr Ile Asn Arg Glu Leu Val Arg Lys Val Asp Gly
 210 215 220
 Lys Ala Gly Leu Val Val His Ser Ser Met Glu Gln Asp Val Gly Leu
 225 230 235 240
 40 Leu Arg Leu Tyr Pro Gly Ile Pro Ala Ala Leu Val Arg Ala Phe Leu
 245 250 255
 Gln Pro Pro Leu Lys Gly Val Val Met Glu Thr Phe Gly Ser Gly Asn
 260 265 270
 Gly Pro Thr Lys Pro Asp Leu Leu Gln Glu Leu Arg Val Ala Thr Glu
 275 280 285
 45 Arg Gly Leu Val Ile Val Asn Cys Thr Gln Cys Leu Arg Gly Ala Val
 290 295 300
 Thr Thr Asp Tyr Ala Ala Gly Met Ala Met Ala Gly Ala Asn Val Ile
 305 310 315 320
 50 Ser Gly Phe Asp Met Thr Ser Glu Ala Ala Leu Ala Lys Leu Ser Tyr
 325 330 335
 Val Leu Gly Gln Pro Gly Leu Ser Leu Asp Val Arg Lys Glu Leu Leu
 340 345 350
 Thr Lys Asp Leu Arg Gly Glu Met Thr Pro Pro Ser Val
 355 360 365

SEQ ID NO: 7:

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Met Ala Arg Ala Val Gly Pro Glu Arg Arg Leu Leu Ala Val Tyr Thr
 1 5 10 15
 Gly Gly Thr Ile Gly Met Arg Ser Glu Leu Gly Val Leu Val Pro Gly
 20 25 30
 Thr Gly Leu Ala Ala Ile Leu Arg Thr Leu Pro Met Phe His Asp Glu
 35 40 45
 Glu His Ala Arg Ala Arg Gly Leu Ser Glu Asp Thr Leu Val Leu Pro
 50 55 60
 Pro Asp Ser Arg Asn Gln Arg Ile Leu Tyr Thr Val Leu Glu Cys Gln
 65 70 75 80
 Pro Leu Phe Asp Ser Ser Asp Met Thr Ile Ala Glu Trp Val Arg Val
 85 90 95
 Ala Gln Thr Ile Lys Arg His Tyr Glu Gln Tyr His Gly Phe Val Val
 100 105 110
 Ile His Gly Thr Asp Thr Met Ala Phe Ala Ala Ser Met Leu Ser Phe
 115 120 125
 Met Leu Glu Asn Leu Gln Lys Thr Val Ile Leu Thr Gly Ala Gln Val
 130 135 140
 Pro Ile His Ala Leu Trp Ser Asp Gly Arg Glu Asn Leu Leu Gly Ala
 145 150 155 160
 Leu Leu Met Ala Gly Gln Tyr Val Ile Pro Glu Val Cys Leu Phe Phe
 165 170 175
 Gln Asn Gln Leu Phe Arg Gly Asn Arg Ala Thr Lys Val Asp Ala Arg
 180 185 190
 Arg Phe Ala Ala Phe Cys Ser Pro Asn Leu Leu Pro Leu Ala Thr Val
 195 200 205
 Gly Ala Asp Ile Thr Ile Asn Arg Glu Leu Val Arg Lys Val Asp Gly
 210 215 220
 Lys Ala Gly Leu Val Val His Ser Ser Met Glu Gln Asp Val Gly Leu
 225 230 235 240
 Leu Arg Leu Tyr Pro Gly Ile Pro Ala Ala Leu Val Arg Ala Phe Leu
 245 250 255
 Gln Pro Pro Leu Lys Gly Val Val Met Glu Thr Phe Gly Ser Gly Asn
 260 265 270
 Gly Pro Thr Lys Pro Asp Leu Leu Gln Glu Leu Arg Val Ala Thr Glu
 275 280 285
 Arg Gly Leu Val Ile Val Asn Cys Thr Gln Cys Leu Arg Gly Ala Val
 290 295 300
 Thr Thr Asp Tyr Ala Ala Gly Met Ala Met Ala Gly Ala Gly Val Ile
 305 310 315 320
 Ser Gly Phe Asp Met Thr Ser Glu Ala Ala Leu Ala Lys Leu Ser Tyr
 325 330 335
 Val Leu Gly Gln Pro Gly Leu Ser Leu Asp Val Arg Lys Glu Leu Leu
 340 345 350
 Thr Lys Asp Leu Arg Gly Glu Met Thr Pro Pro Ser Val
 355 360 365

SEQ ID NO: 8:

5 Met Ala Arg Ala Val Gly Pro Glu Arg Arg Leu Leu Ala Val Tyr Thr
 1 5 10 15
 Gly Gly Thr Ile Gly Met Arg Ser Glu Leu Gly Val Leu Val Pro Gly
 20 25 30
 10 Thr Gly Leu Ala Ala Ile Leu Arg Thr Leu Pro Met Phe His Asp Glu
 35 40 45

 15 Glu His Ala Arg Ala Arg Gly Leu Ser Glu Asp Thr Leu Val Leu Pro
 50 55 60
 Pro Asp Ser Arg Asn Gln Arg Ile Leu Tyr Thr Val Leu Glu Cys Gln
 65 70 75 80
 20 Pro Leu Phe Asp Ser Ser Asp Met Thr Ile Ala Glu Trp Val Arg Val
 85 90 95
 Ala Gln Thr Ile Lys Arg His Tyr Glu Gln Tyr His Gly Phe Val Val
 100 105 110
 Ile His Gly Thr Asp Thr Met Ala Phe Ala Ala Ser Met Leu Ser Phe
 115 120 125
 25 Met Leu Glu Asn Leu Gln Lys Thr Val Ile Leu Thr Gly Ala Gln Val
 130 135 140
 Pro Ile His Ala Leu Trp Ser Asp Gly Arg Glu Asn Leu Leu Gly Ala
 145 150 155 160
 Leu Leu Met Ala Gly Gln Tyr Val Ile Pro Glu Val Cys Leu Phe Phe
 165 170 175
 30 Gln Asn Gln Leu Phe Arg Gly Asn Arg Ala Thr Lys Val Asp Ala Arg
 180 185 190
 Arg Phe Ala Ala Phe Cys Ser Pro Asn Leu Leu Pro Leu Ala Thr Val
 195 200 205
 35 Gly Ala Asp Ile Thr Ile Asn Arg Glu Leu Val Arg Lys Val Asp Gly
 210 215 220
 Lys Ala Gly Leu Val Val His Ser Ser Met Glu Gln Asp Val Gly Leu
 225 230 235 240
 Leu Arg Leu Tyr Pro Gly Ile Pro Ala Ala Leu Val Arg Ala Phe Leu
 245 250 255
 40 Gln Pro Pro Leu Lys Gly Val Val Met Glu Thr Phe Gly Ser Gly Asn
 260 265 270
 Gly Pro Thr Lys Pro Asp Leu Leu Gln Glu Leu Arg Val Ala Thr Glu
 275 280 285
 Arg Gly Leu Val Ile Val Asn Cys Thr Gln Cys Leu Gln Gly Ala Val
 290 295 300
 45 Thr Thr Asp Tyr Ala Ala Gly Met Ala Met Ala Gly Ala Asn Val Ile
 305 310 315 320
 Ser Gly Phe Asp Met Thr Ser Glu Ala Ala Leu Ala Lys Leu Ser Tyr
 325 330 335
 50 Val Leu Gly Gln Pro Gly Leu Ser Leu Asp Val Arg Lys Glu Leu Leu
 340 345 350
 Thr Lys Asp Leu Arg Gly Glu Met Thr Pro Pro Ser Val
 355 360 365

SEQ ID NO: 9:

5 Met Ala Arg Ala Val Gly Pro Glu Arg Arg Leu Leu Ala Val Tyr Thr
 1 5 10 15
 Gly Gly Thr Ile Gly Met Arg Ser Glu Leu Gly Val Leu Val Pro Gly
 20 25 30
 Thr Gly Leu Ala Ala Ile Leu Arg Thr Leu Pro Met Phe His Asp Glu
 35 40 45
 10 Glu His Ala Arg Ala Arg Gly Leu Ser Glu Asp Thr Leu Val Leu Pro
 50 55 60
 Pro Asp Ser Arg Asn Gln Arg Ile Leu Tyr Thr Val Leu Glu Cys Gln
 65 70 75 80
 15 Pro Leu Phe Asp Ser Ser Asp Met Thr Ile Ala Glu Trp Val Arg Val
 85 90 95

20 Ala Gln Thr Ile Lys Arg His Tyr Glu Gln Tyr His Gly Phe Val Val
 100 105 110
 Ile His Gly Thr Asp Thr Met Ala Phe Ala Ala Ser Met Leu Ser Phe
 115 120 125
 Met Leu Glu Asn Leu Gln Lys Thr Val Ile Leu Thr Gly Ala Gln Val
 130 135 140
 25 Pro Ile His Ala Leu Trp Ser Asp Gly Arg Glu Asn Leu Leu Gly Ala
 145 150 155 160
 Leu Leu Met Ala Gly Gln Tyr Val Ile Pro Glu Val Cys Leu Phe Phe
 165 170 175
 30 Gln Asn Gln Leu Phe Arg Gly Asn Arg Ala Thr Lys Val Asp Ala Arg
 180 185 190
 Arg Phe Ala Ala Phe Cys Ser Pro Asn Leu Leu Pro Leu Ala Thr Val
 195 200 205
 Gly Ala Asp Ile Thr Ile Asn Arg Glu Leu Val Arg Lys Val Asp Gly
 210 215 220
 35 Lys Ala Gly Leu Val Val His Ser Ser Met Glu Gln Asp Val Gly Leu
 225 230 235 240
 Leu Arg Leu Tyr Pro Gly Ile Pro Ala Ala Leu Val Arg Ala Phe Leu
 245 250 255
 40 Gln Pro Pro Leu Lys Gly Val Val Met Glu Thr Phe Gly Ser Gly Asn
 260 265 270
 Gly Pro Thr Lys Pro Asp Leu Leu Gln Glu Leu Arg Val Ala Thr Glu
 275 280 285
 Arg Gly Leu Val Ile Val Asn Cys Thr Gln Cys Leu Gln Gly Ala Val
 290 295 300
 45 Thr Thr Asp Tyr Ala Ala Gly Met Ala Met Ala Gly Ala Gly Val Ile
 305 310 315 320
 Ser Gly Phe Asp Met Thr Ser Glu Ala Ala Leu Ala Lys Leu Ser Tyr
 325 330 335
 Val Leu Gly Gln Pro Gly Leu Ser Leu Asp Val Arg Lys Glu Leu Leu
 340 345 350
 50 Thr Lys Asp Leu Arg Gly Glu Met Thr Pro Pro Ser Val.
 355 360 365

55 5. The polypeptide of claim 1, which originates from a member selected from the group consisting of guinea pig and human.

6. The polypeptide of claim 1, which exists in the form of an oligomer.

7. A DNA which encodes the polypeptide as claimed in claim 1.
8. The DNA of claim 7, which contains a nucleotide sequence selected from the group consisting of SEQ ID NOs:10 to 14, their homologous ones, and complementary ones thereunto;

SEQ ID NO:10

10 ATGGCGCGCG CATCAGGCTC CGAGAGGCAC CTGCTGCTCA TCTACACTGG CGGCACTTTG 60
 GGCATGCAGA GCAAGGGCGG GGTGCTCGTC CCCGGGCCAG GCCTGGTCAC TCTGCTGCGG 120
 ACCCTGCCCCA TGTTCCATGA CAAGGAGTTC GCCCAGGCC AGGGCCTCCC TGACCATGCT 180
 CTGGCGCTGC CCCCTGCCAG CCACGGCCCC AGGGTCCTCT ACACGGTGCT GGAGTGCCAG 240
 CCCCTCTTGG ATTCCAGCGA CATGACCATC GATGATTGGA TTCGCATAGC CAAGATCATA 300
 15 GAGAGGCACT ATGAGCAGTA CCAAGGCTTT GTGGTTATCC ACGGCACCGA CACCATGGCC 360
 TTTGGGGCCT CCATGCTGTC CTTTCATGCTG GAAAACCTGC ACAAACCACT CATCCTCACT 420
 GGCGCCCAGG TGCCAATCCG TGTGCTGTGG AATGACGCCC GGGAAAACCT GCTGGGGGCG 480
 TTGCTTGTGG CCGGCCAATA CATCATCCCT GAGGTCTGCC TGTATTATGAA CAGTCAGCTG 540
 TTTGCGGGAA ACCGGGTAAC CAAGGTGGAC TCCCAGAAGT TTGAGGCCTT CTGCTCCCCC 600
 AATCTGTCCC CACTAGCCAC TGTGGGCGCG GATGTCACAA TTGCCTGGGA CCTGGTGCGC 660
 20 AAGGTCAACT GGAAGGACCC GCTGGTGGTG CACAGCAACA TGGAGCACGA CGTGGCACTG 720
 CTGCGCCTCT ACCCTGGCAT CCCGGCCTCC CTGGTCCGGG CATTCCTGCA GCCCCGCTC 780
 AAGGGCGTGG TCCTGGAGAC CTTTCGGCTCT GGCAACGGGC CGAGCAAGCC CGACCTGCTG 840
 CAGGAGTTGC GGGCCGCGGC CCAGCGCGGC CTCATCATGG TCAACTGCAG CCAGTGCCTG 900
 CGGGGGTCTG TGACCCCGGG CTATGCCACG AGCTTGGCGG GCGCCAACAT CGTGTCCGGC 960
 25 TTAGACATGA CCTCAGAGGC CGCGCTGGCT AAGCTGTCCT ACGTGTGGG CCTGCCGGAG 1020
 CTGAGCCTGG AGCGCAGGCA GGAGCTGCTG GCCAAGGATC TTCGCGGGGA AATGACACTG 1080
 CCCACGGCA 1089

SEQ ID NO: 11:

ATGGCGCGCG CGGTGGGGCC CGAGCGGAGG CTGCTGGCCG TCTACACCGG CGGCACCATT 60
 GGCATGCGGA GTGAGCTCGG CGTGCTTGTG CCCGGGACGG GCCTGGCTGC CATCCTGAGG 120
 35 AACTGCCCCA TGTTCCATGA CGAGGAGCAC GCCCGAGCCC GCGGCCCTCTC TGAGGACACC 180
 CTGGTGCTAC CCCCGACAG CCGCAACCAG AGGATCCTCT ACACCGTGCT GGAGTGCCAG 240
 CCCCTCTTCG ACTCCAGTGA CATGACCATC GCTGAGTGGG TTCGCGTTGC CCAGACCATC 300
 AAGAGGCACT ACAGCAGTA CCACGGCTTT GTGGTCATCC ACGGCACCGA CACCATGGCC 360
 TTTGCTGCCT CGATGCTGTC CTTTCATGCTG GAGAACCTGC AGAAGACTGT CATCCTCACT 420
 40 GGGGCCCAGG TGCCCATCCA TGCCCTGTGG AGCGACGGCC GTGAGAACCT GCTGGGGGCA 480
 CTGCTCATGG CTGGCCAGTA TGTGATCCCA GAGGTCTGCC TTTTCTTCCA GAATCAGCTG 540
 TTTGCGGGCA ACCGGGCAAC CAAGGTAGAC GCTCGGAGGT TCGCAGCTTT CTGCTCCCCG 600
 AACCTGCTGC CTCTGGCCAC AGTGGGTGCT GACATCACAA TCAACAGGGA GCTGGTGCGG 660
 AAGGTGGACG GGAAGGCTGG GCTGGTGGTG CACAGCAGCA TGGAGCAGGA CGTGGGCCTG 720
 CTGCGCCTCT ACCCTGGGAT CCCTGCCGCC CTGGTTCGGG CCTTCTTGCA GCCTCCCCG 780
 45 AAGGGCGTGG TCATGGAGAC CTTTCGGTTCA GGAACGGAC CCACCAAGCC CGACCTGCTG 840
 CAGGAGCTGC GGGTGGCCAC CGAGCGCGGC CTGGTCATCG TCAACTGTAC CCAGTGCCTC 900
 CGGGGGGCTG TGACCACAGA CTATGCAGCT GGCATGGCCA TGGCGGGAGC CAACGTCATC 960
 TCAGGCTTCG ACATGACATC GGAGGCCGCC CTGGCCAAGC TATCGTATGT GCTGGGCCAG 1020
 CCAGGGCTGA GCCTGGATGT CAGGAAGGAG CTGCTGACCA AGGACCTTCG GGGGGAGATG 1080
 50 ACGCCACCCT CGGTG 1095

SEQ ID NO: 12:

5 ATGGCGCGCG CGGTGGGGCC CGAGCGGAGG CTGCTGGCCG TCTACACCGG CGGCACCATT 60
 GGCATGCGGA GTGAGCTCGG CGTGCTTGTG CCCGGGACGG GCCTGGCTGC CATCCTGAGG 120
 ACACTGCCCA TGTTCCATGA CGAGGAGCAC GCCCGAGCCC GCGGCCTCTC TGAGGACACC 180
 CTGGTGCTAC CCCC GGACAG CCGCAACCAG AGGATCCTCT ACACCGTGCT GGAGTGCCAG 240
 CCCCTCTTCG ACTCCAGTGA CATGACCATC GCTGAGTGGG TTCGCGTTGC CCAGACCATC 300
 AAGAGGCACT ACGAGCAGTA CCACGGCTTT GTGGTCATCC ACGGCACCGA CACCATGGCC 360
 10
 15 TTTGCTGCCT CGATGCTGTC CTTCATGCTG GAGAACCTGC AGAAGACTGT CATCCTCACT 420
 GGGGCCCAGG TGCCCATCCA TGCCCTGTGG AGCGACGGCC GTGAGAACCT GCTGGGGGCA 480
 CTGCTCATGG CTGGCCAGTA TGTGATCCCA GAGGTCTGCC TTTTCTTCCA GAATCAGCTG 540
 TTTCGGGGCA ACCGGGCAAC CAAGGTAGAC GCTCGGAGGT TCGCAGCTTT CTGCTCCCCG 600
 AACCTGCTGC CTCTGGCCAC AGTGGGTGCT GACATCACA TCAACAGGGA GCTGGTGCGG 660
 AAGGTGGACG GGAAGGCTGG GCTGGTGGTG CACAGCAGCA TGGAGCAGGA CGTGGGCCTG 720
 CTGCGCCTCT ACCCTGGGAT CCCTGCCGCC CTGGTTCGGG CCTTCTTGCA GCCTCCCCCTG 780
 20 AAGGGCGTGG TCATGGAGAC CTTTCGGTTCA GGAACGGAC CCACCAAGCC CGACCTGCTG 840
 CAGGAGCTGC GGGTGGCCAC CGAGCGCGGC CTGGTCATCG TCAACTGTAC CCAGTGCCCTC 900
 CGGGGGGCTG TGACCACAGA CTATGCAGCT GGCATGGCCA TGGCGGGAGC CGGCGTCATC 960
 TCAGGCTTCG ACATGACATC GGAGGCCGCC CTGGCCAAGC TATCGTATGT GCTGGGCCAG 1020
 CCAGGGCTGA GCCTGGATGT CAGGAAGGAG CTGCTGACCA AGGACCTTCG GGGGGAGATG 1080
 25 ACGCCACCCT CGGTG 1095

SEQ ID NO: 13:

30 ATGGCGCGCG CGGTGGGGCC CGAGCGGAGG CTGCTGGCCG TCTACACCGG CGGCACCATT 60
 GGCATGCGGA GTGAGCTCGG CGTGCTTGTG CCCGGGACGG GCCTGGCTGC CATCCTGAGG 120
 ACACTGCCCA TGTTCCATGA CGAGGAGCAC GCCCGAGCCC GCGGCCTCTC TGAGGACACC 180
 35 CTGGTGCTAC CCCC GGACAG CCGCAACCAG AGGATCCTCT ACACCGTGCT GGAGTGCCAG 240
 CCCCTCTTCG ACTCCAGTGA CATGACCATC GCTGAGTGGG TTCGCGTTGC CCAGACCATC 300
 AAGAGGCACT ACGAGCAGTA CCACGGCTTT GTGGTCATCC ACGGCACCGA CACCATGGCC 360
 TTTGCTGCCT CGATGCTGTC CTTCATGCTG GAGAACCTGC AGAAGACTGT CATCCTCACT 420
 GGGGCCCAGG TGCCCATCCA TGCCCTGTGG AGCGACGGCC GTGAGAACCT GCTGGGGGCA 480
 40 CTGCTCATGG CTGGCCAGTA TGTGATCCCA GAGGTCTGCC TTTTCTTCCA GAATCAGCTG 540
 TTTCGGGGCA ACCGGGCAAC CAAGGTAGAC GCTCGGAGGT TCGCAGCTTT CTGCTCCCCG 600
 AACCTGCTGC CTCTGGCCAC AGTGGGTGCT GACATCACA TCAACAGGGA GCTGGTGCGG 660
 AAGGTGGACG GGAAGGCTGG GCTGGTGGTG CACAGCAGCA TGGAGCAGGA CGTGGGCCTG 720
 CTGCGCCTCT ACCCTGGGAT CCCTGCCGCC CTGGTTCGGG CCTTCTTGCA GCCTCCCCCTG 780
 AAGGGCGTGG TCATGGAGAC CTTTCGGTTCA GGAACGGAC CCACCAAGCC CGACCTGCTG 840
 45 CAGGAGCTGC GGGTGGCCAC CGAGCGCGGC CTGGTCATCG TCAACTGTAC CCAGTGCCCTC 900
 CAGGGGGCTG TGACCACAGA CTATGCAGCT GGCATGGCCA TGGCGGGAGC CAACGTCATC 960
 TCAGGCTTCG ACATGACATC GGAGGCCGCC CTGGCCAAGC TATCGTATGT GCTGGGCCAG 1020
 CCAGGGCTGA GCCTGGATGT CAGGAAGGAG CTGCTGACCA AGGACCTTCG GGGGGAGATG 1080
 ACGCCACCCT CGGTG 1095
 50
 55

SEQ ID NO: 14:

5 ATGGCGCGCG CGGTGGGGCC CGAGCGGAGG CTGCTGGCCG TCTACACCGG CGGCACCATT 60
 GGCATGCGGA GTGAGCTCGG CGTGCTTGTC CCCGGGACGG GCCTGGCTGC CATCCTGAGG 120
 AACTGCCCA TGTTCATGA CGAGGAGCAC GCCCGAGCCC GCGGCCTCTC TGAGGACACC 180
 CTGGTGCTAC CCCCAGACAG CCGCAACCAG AGGATCCTCT ACACCGTGCT GGAGTGCCAG 240
 CCCCTCTTCG ACTCCAGTGA CATGACCATC GCTGAGTGGG TTCGCGTTGC CCAGACCATC 300
 10 AAGAGGCACT ACGAGCAGTA CCACGGCTTT GTGGTCATCC ACGGCACCGA CACCATGGCC 360
 TTTGCTGCCT CGATGCTGTC CTTTCATGCTG GAGAACCTGC AGAAGACTGT CATCCTCACT 420
 GGGGCCAGG TGCCCATCCA TGCCCTGTGG AGCGACGGCC GTGAGAACCT GCTGGGGGCA 480
 CTGCTCATGG CTGGCCAGTA TGTGATCCCA GAGGTCTGCC TTTTCTTCCA GAATCAGCTG 540
 TTTCCGGGCA ACCGGGCAAC CAAGGTAGAC GCTCGGAGGT TCGCAGCTTT CTGCTCCCCG 600
 AACCTGCTGC CTCTGGCCAC AGTGGGTGCT GACATCAAA TCAACAGGGA GCTGGTGCCG 660
 15 AAGGTGGACG GGAAGGCTGG GCTGGTGGT CACAGCAGCA TGGAGCAGGA CGTGGGCCTG 720
 CTGCGCCTCT ACCCTGGGAT CCCTGCCGCC CTGGTTCGGG CTTTCTTGCA GCCTCCCCTG 780
 AAGGGCGTGG TCATGGAGAC CTTCCGGTTC GGGAACGGAC CCACCAAGCC CGACCTGCTG 840
 CAGGAGCTGC GGGTGGCCAC CGAGCGCGGC CTGGTCATCG TCAACTGTAC CCAGTGCCTC 900

20
 CAGGGGGCTG TGACCACAGA CTATGCAGCT GGCATGGCCA TGGCGGGAGC CGGCGTCATC 960
 TCAGGCTTCG ACATGACATC GGAGGCCGCC CTGGCCAAGC TATCGTATGT GCTGGGCCAG 1020
 25 CCAGGGCTGA GCCTGGATGT CAGGAAGGAG CTGCTGACCA AGGACCTTCG GGGGGAGATG 1080
 ACCCCACCCT CGGTG 1095.

9. The DNA of claim 7, which originates from a member selected from the group consisting of guinea pig and human.
- 30 10. A self-replicable vector which contains a DNA encoding the polypeptide as claimed in claim 1.
11. The self-replicable vector of claim 10, which is a plasmid vector.
12. The self-replicable vector of claim 10, which contains one or more members selected from the group consisting of metallothionein and Tac promoters.
- 35 13. A transformant obtainable by introducing the DNA of claim 7 into a host.
14. The transformant of claim 13, wherein said host is a member selected from the group consisting of prokaryotic and eukaryotic cells.
- 40 15. The transformant of claim 13, wherein said host is *Escherichia coli*.
16. The transformant of claim 13, wherein said host is a mouse cell.
- 45 17. A transformant obtainable by the self replicable vector of claim 10 into a host.
18. The transformant of claim 17, wherein said host is a member selected from the group consisting of prokaryotic and eukaryotic cells.
- 50 19. The transformant of claim 17, wherein said host is *Escherichia coli*.
20. The transformant of claim 17, wherein said host is a mouse cell.
- 55 21. A process for preparing a polypeptide, which comprises (a) artificially expressing a DNA encoding the polypeptide of claim 1, and (b) collecting the polypeptide from the resultant mixture.
22. The process of claim 21, wherein the artificial expression of the step (a) contains culturing the transformant of

claim 13.

23. The process of claim 21, wherein the artificial expression of the step (a) contains culturing the transformant of claim 17.

24. The process of claim 21, wherein the resultant mixture of the step (b) is a culture of the transformant of claim 13.

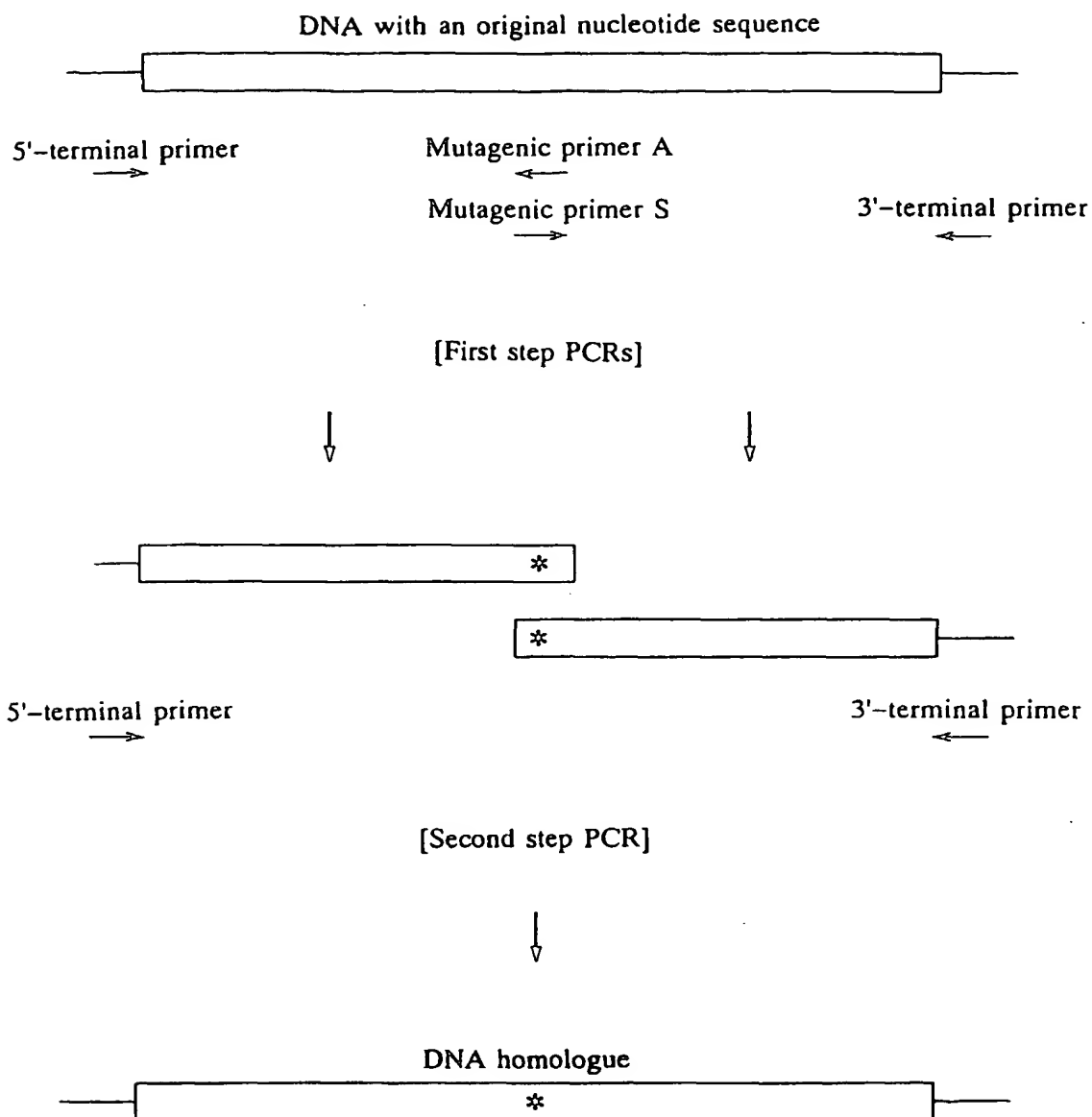
25. The process of claim 21, wherein the resultant mixture of the step (b) is a culture of the transformant of claim 17.

26. The process of claim 21, wherein the polypeptide is collected by one or more techniques selected from the group consisting of salting out, dialysis, filtration, concentration, gel filtration chromatography, ion-exchange chromatography, affinity chromatography, hydrophobic chromatography, isoelectric focusing and gel electrophoresis.

27. An agent for susceptible diseases, which contains the polypeptide of claim 1 as an effective ingredient.

28. The agent of claim 27, wherein said diseases are malignant tumors, leukemias and lymphomas.

29. The agent of claim 27, which contains one or more members selected from the group consisting of serum albumin, glycerol, gelatin, trehalose and maltose as a stabilizer.



Note: An asterisk indicates a site where a nucleotide is substituted, and a box indicates a polypeptide-encoding sequence.

FIG.1

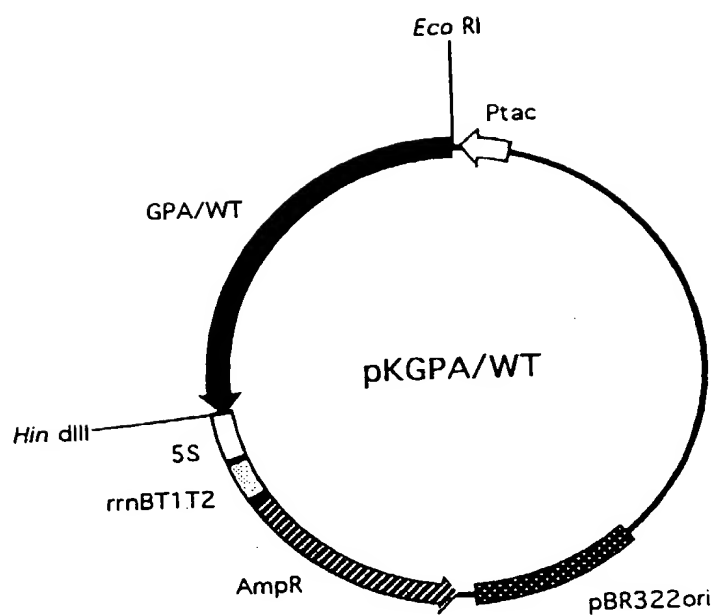


FIG.2

Template DNA : pCGPA/WT
 Sense primer : 5' -GTGAATTCGGAGGTTTCAGATGGCGCGGCATCA-3'
 Anti-sense primer : 5' -CTGCGGCCGCTCAGATGGCAGGCGGCAC-3'

↓ PCR

Amplified DNA

↓ Cleavage by *Bco* RI and *Not* I

DNA fragment about 1.7 kbp in length

Linkers :

5' -TCGAGCCACCATGAAGTGTTCGTGGGTATT-3'

5' -TTCTTCCTGATGGCCGTAGTGACAGGAGTG-3'

5' -AATTCACCTCTGTCACTACGGCCATCAGGA-3'

5' -AGAAAATAACCCACGAACACTTCATGGTGGC-3'

↓ Phosphorylation
 by T4 polynucleotide kinase

5'-terminal phosphorylated linkers

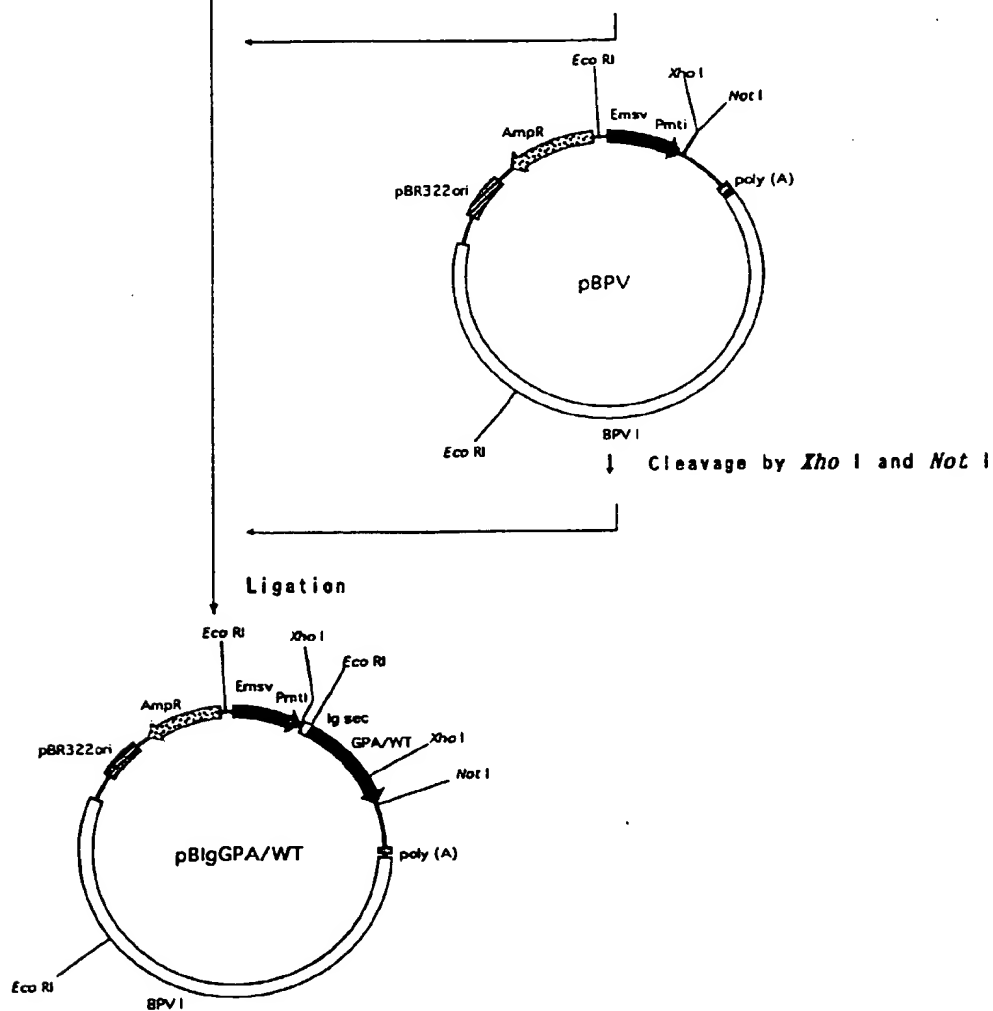


FIG.3

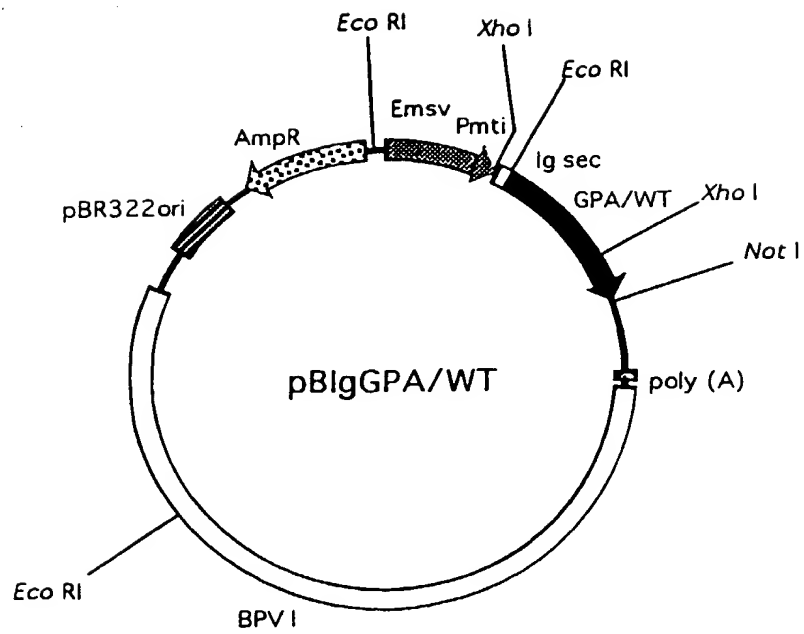


FIG.4

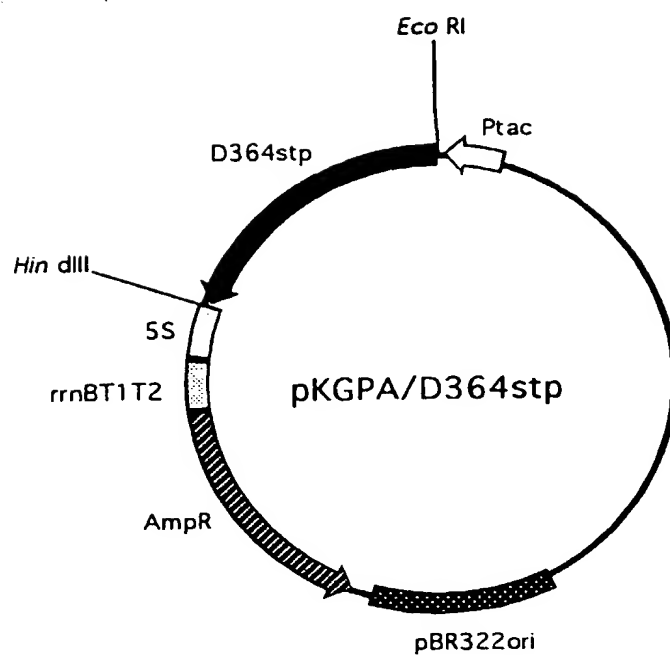


FIG.5

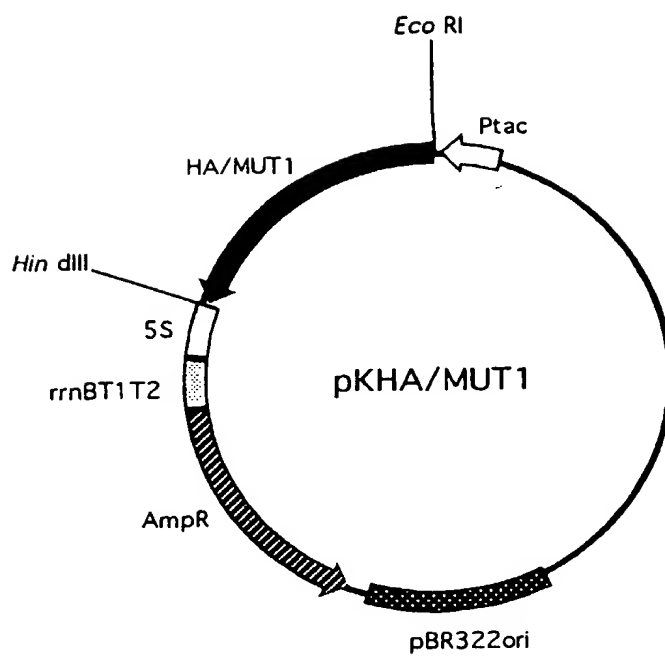


FIG.6

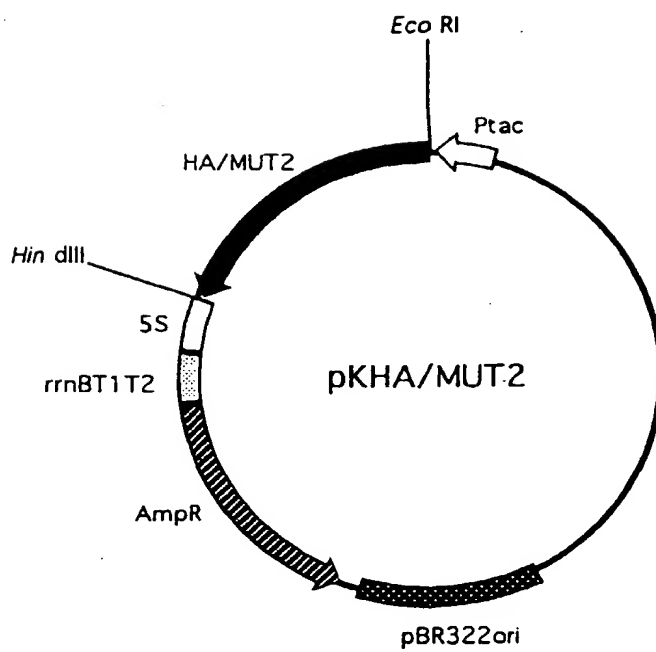


FIG.7

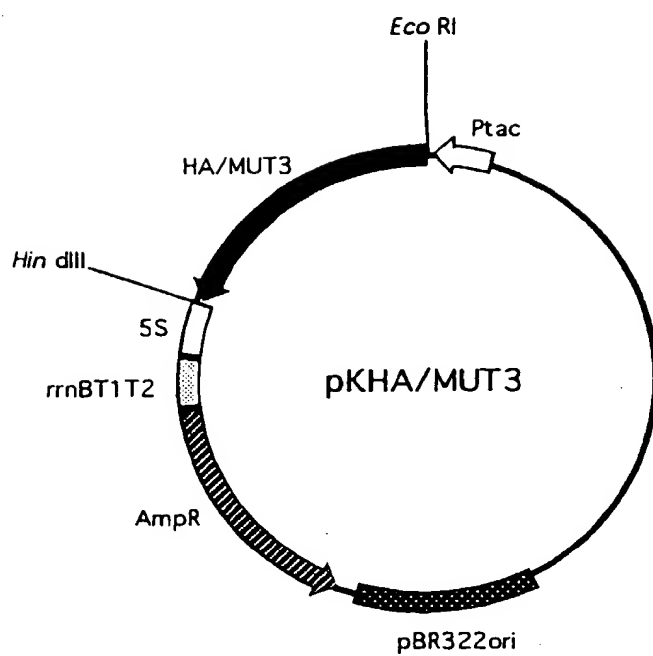


FIG.8

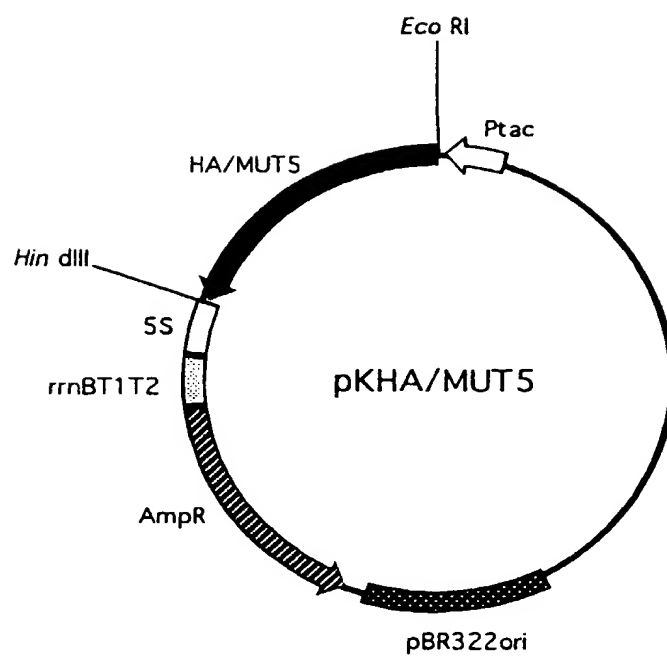


FIG.9

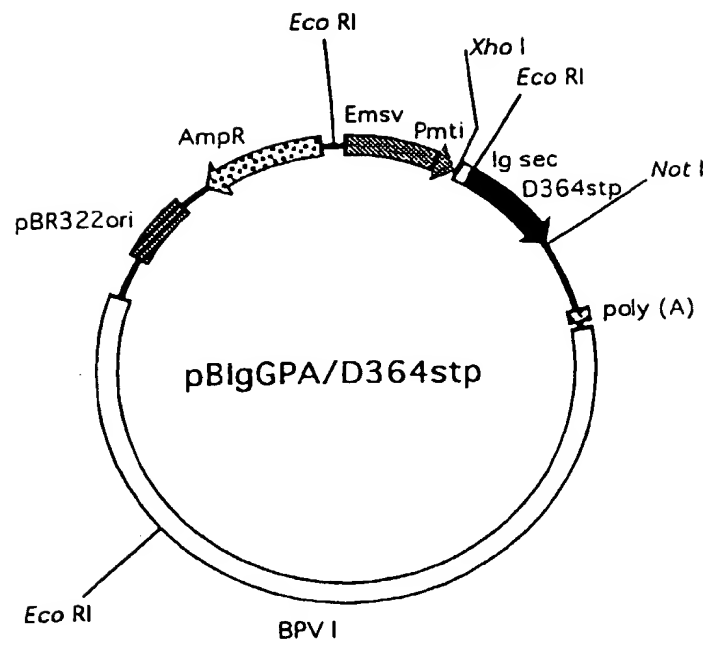


FIG.10

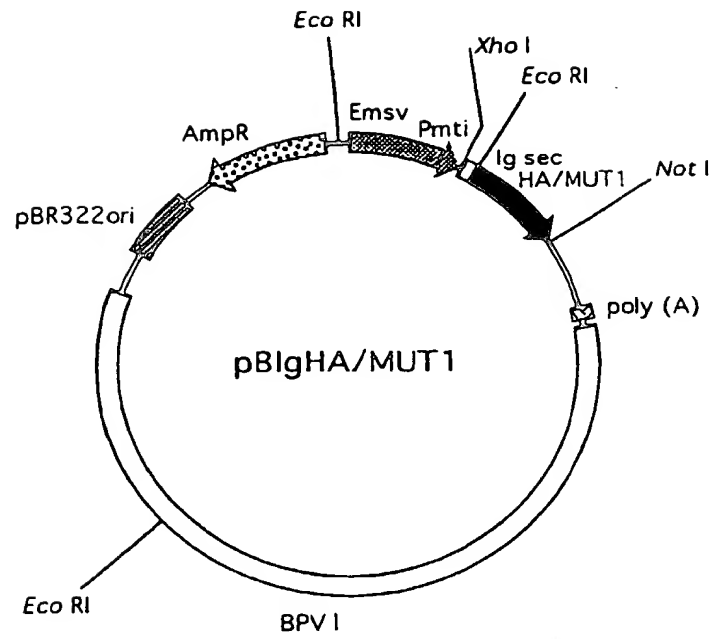


FIG.11

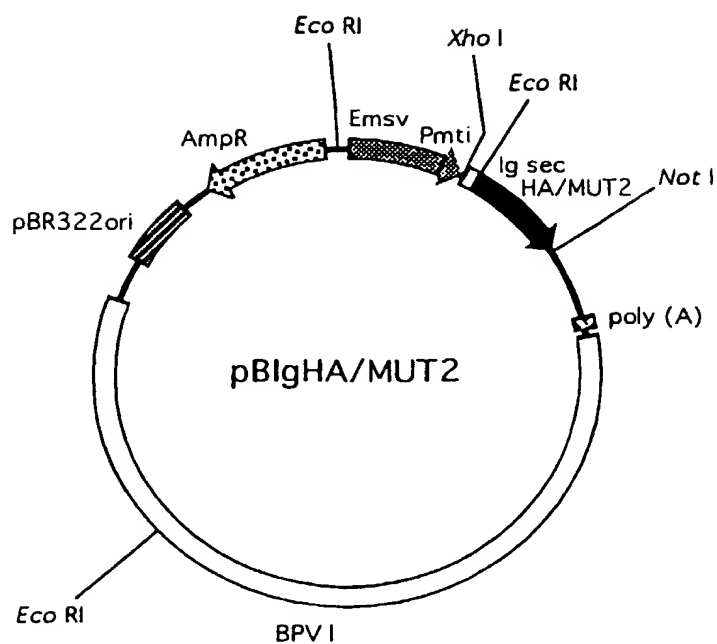


FIG.12

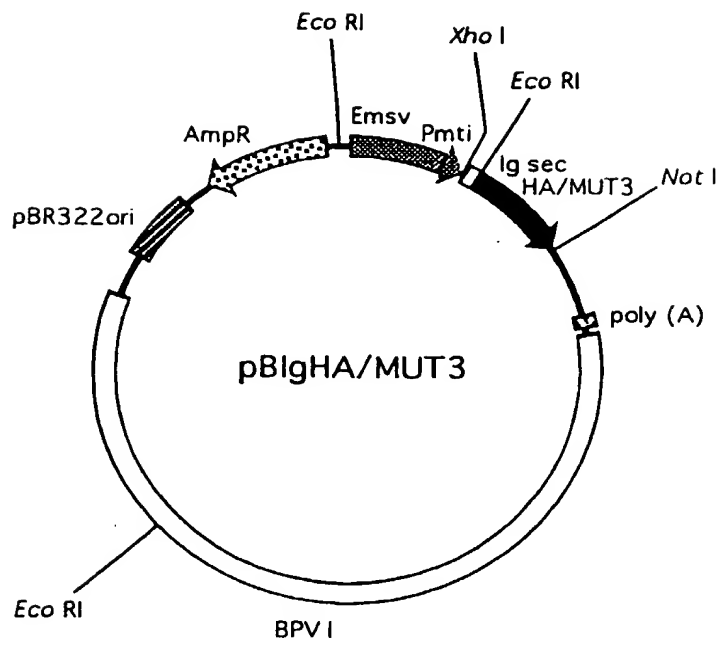


FIG.13

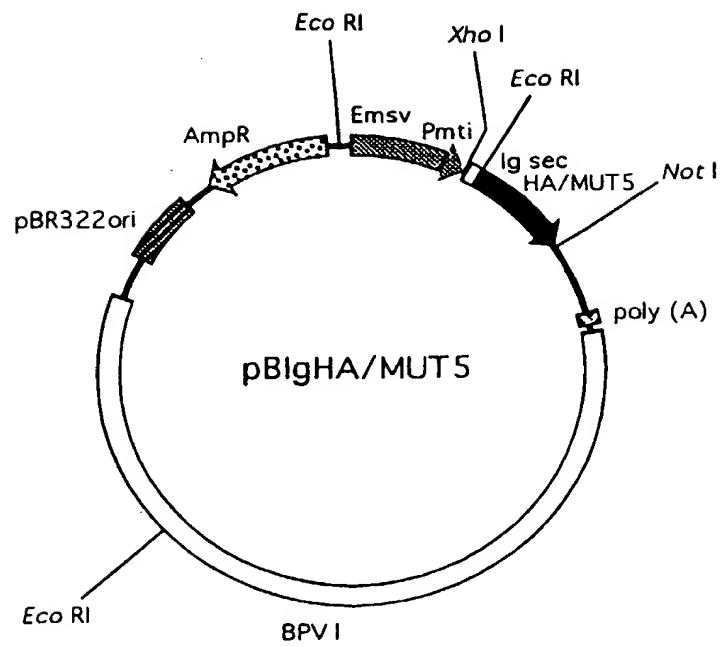


FIG.14



(19)



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(71) Applicant: **KABUSHIKI KAISHA HAYASHIBARA
SEIBUTSU KAGAKU KENKYUJO
Okayama-shi Okayama (JP)**

(72) Inventors:
• **Ario, Takeshi
Okayama-shi, Okayama (JP)**

• **Taniai, Madoka
Okayama-shi, Okayama (JP)**
• **Yamamoto, Kozo
Okayama-shi, Okayama (JP)**
• **Kurimoto, Masashi
Okayama-shi, Okayama (JP)**

(74) Representative: **Daniels, Jeffrey Nicholas et al
Page White & Farrer
54 Doughty Street
London WC1N 2LS (GB)**

(54) Polypeptides having L-asparaginase activity

(57) Disclosed are polypeptides which originate from mammal, having L-asparaginase activity. The polypeptides are easily prepared by applying recombinant DNA techniques to DNAs encoding the polypeptides and they exert satisfactory effects in the treatment and/or the prevention for diseases caused by tumor cells dependent on L-asparagine, and cause no substantial serious side effects even when administered to humans in relatively-high dose.

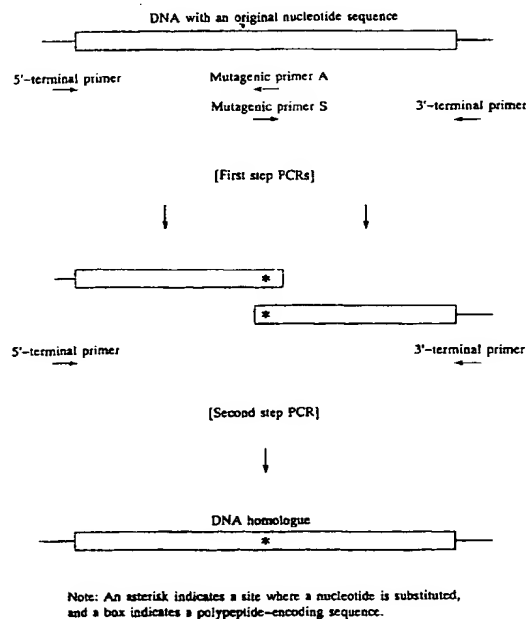


FIG.1



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Office

EUROPEAN SEARCH REPORT

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DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION' (Int.Cl.6)
X,P	EP 0 726 313 A (HAYASHIBARA BIOCHEM LAB) 14 August 1996 * the whole document *	1-11, 13-15, 17-19, 21-25, 27,28	C12N15/55 C12N9/82 C12N15/70 C12N15/79 C12N1/21 C12N5/10 A61K38/46 //(C12N1/21, C12R1:19)
X	YELLIN T O ET AL: "PURIFICATION AND PROPERTIES OF GUINIEA PIG SERUM ASPARAGINASE" BIOCHEMISTRY, vol. 5, no. 5, May 1966, pages 1605-1612, XP002012974 * the whole document *	1-29	
X	PATENT ABSTRACTS OF JAPAN vol. 004, no. 046 (C-006), 10 April 1980 & JP 55 019018 A (TOUBISHI YAKUHI KOGYO KK), 9 February 1980 * abstract *	1,2,4-29	
X	PATENT ABSTRACTS OF JAPAN vol. 017, no. 158 (C-1041), 29 March 1993 & JP 04 320684 A (JAPAN SYNTHETIC RUBBER CO LTD), 11 November 1992 * abstract *	1,2,4-29	TECHNICAL FIELDS SEARCHED (Int.Cl.6) C12N
The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 7 September 1998	Examiner Fernandez y Branas, F
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